

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 01:20:34 ; Search time 1776.4 Seconds
(without alignments)
11108.167 Million cell updates/sec

Title: US-09-555-093-1
Perfect score: 1462
Sequence: 1 gctcaccacaaatgtgtctgc.....ataaaacctgttttcaa 1462

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- EST:*
- 1: em_estba:*
 - 2: em_esthum:*
 - 3: em_estin:*
 - 4: em_estmu:*
 - 5: em_estov:*
 - 6: em_estpl:*
 - 7: em_estro:*
 - 8: em_htc:*
 - 9: gb_est1:*
 - 10: gb_est2:*
 - 11: gb_htc:*
 - 12: gb_gss:*
 - 13: em_gss_hum:*
 - 14: em_gss_inv:*
 - 15: em_gss_pln:*
 - 16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	743.4	50.8	773	10	BJ153638
c 2	736.4	50.4	746	10	BJ139067
c 3	736.4	50.4	761	10	BJ129368
c 4	733.8	50.2	763	10	BJ149952
c 5	731.4	50.0	756	10	BJ128883
c 6	727.4	49.8	743	10	BJ128630
c 7	724.8	49.6	742	10	BJ129934
c 8	724.4	49.5	751	10	BJ146824
c 9	724.2	49.5	748	10	BJ134106
c 10	722.2	49.4	750	10	BJ148511
c 11	719.6	49.2	762	10	BJ128407
c 12	707	48.4	731	10	BJ149141
c 13	704.4	48.2	720	9	AU210015
c 14	702.8	48.1	721	10	BJ151779
c 15	701.8	48.0	725	10	BJ152662
c 16	701.8	48.0	727	9	AU213941
c 17	694.6	47.5	719	9	AU213658

c 18	693	47.4	720	10	BJ130441	BJ130441
c 19	682	46.6	705	10	BJ140668	BJ140668
c 20	677.4	46.3	695	10	BJ128927	BJ128927
c 21	675.8	46.2	689	10	BJ131677	BJ131677
c 22	675.2	46.2	686	10	BJ138657	BJ138657
c 23	674.4	46.1	704	10	BJ137106	BJ137106
c 24	665	45.5	689	9	AU209976	AU209976
c 25	662.8	45.3	696	10	BJ122807	BJ122807
c 26	657	44.9	682	10	BJ130694	BJ130694
c 27	641.2	43.9	672	10	BJ151152	BJ151152
c 28	639.2	43.7	671	10	BJ134613	BJ134613
c 29	636.2	43.5	655	10	BJ144819	BJ144819
c 30	635.4	43.5	658	9	AU202072	AU202072
c 31	633.4	43.3	650	9	AU215555	AU215555
c 32	624.4	42.7	627	10	BJ155885	BJ155885
c 33	623.6	42.7	650	10	BJ143820	BJ143820
c 34	621.4	42.5	623	10	BJ120260	BJ120260
c 35	618.6	42.3	639	10	BJ134940	BJ134940
c 36	611.4	41.8	639	10	BJ154428	BJ154428
c 37	600	41.0	637	9	AU218806	AU218806
c 38	598.4	40.9	625	10	BJ136773	BJ136773
c 39	597.4	40.9	614	10	BJ104065	BJ104065
c 40	596.4	40.8	605	9	AU217864	AU217864
c 41	595.8	40.8	618	10	BJ114675	BJ114675
c 42	593.2	40.6	627	10	BJ147665	BJ147665
c 43	592.4	40.5	594	10	BJ103098	BJ103098
c 44	591.6	40.5	618	10	BJ106921	BJ106921
c 45	588.4	40.2	605	10	BJ101261	BJ101261

ALIGNMENTS

RESULT 1
BJ153638/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
BASE COUNT
ORIGIN
Query Match

773 bp mRNA linear EST 24-JAN-2002
BJ153638 unpublished oligo-capped cDNA library, C. elegans LI stage;
Caenorhabditis elegans cDNA clone yk1321f12 3', mRNA sequence.
BJ153638
EST.
BJ153638.1 GI:18321623
Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 773)
Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
A complementary view of the C.elegans genome
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1..773
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk1321f12"
/clone_lib="unpublished oligo-capped cDNA library, C.
elegans LI stage"
/sex="hermaphrodite"
/tissue_type="whole animal"
/dev_stage="L1"

255 a 136 c 160 g 222 t
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Best Local Similarity 99.5%; Pred. NO. 3.3e-127;
Matches 767; Conservative 0; Mismatches 1; Indels 3; Gaps 2;

Qy 690 tcgcatttattccagagatttgcagagataagccagctttgaaaaaacaattctca 749
Db 773 TCGCAATTTATTCAGAGATTGTGCAGTATAAGCCAGCTTTGAAAAGCAATTCICA 714
Qy 750 agattgtaccatacaacatctctatttcacgcgaatgcttccaatgctccgtttctcat 809
Db 713 AGATTGTACCATATCAACATCTATTTCACCGCAATGCTTCCATGCTCCGTTCTCAT 654
Qy 810 ggaatggttcagtcagttcaatgggtatttcaagagatacaaatgaggtacagtctatc 869
Db 653 GGACGTGTCAGTCAGTTCAATGGGTATTCAAGAGAAATCAAAATGAGTACAAAGGTCTATC 594
Qy 870 aaagaaatgcatcttcggagcaagaacaattgttgacattggcgttgcgttatctatc 929
Db 593 AAAGAAATGCAATCTCTGGGAGCAAGCAAAATTTGTTGGACATTTGGGCTTGGGTATTCATTC 534
Qy 930 aattgtcttattacacatggccacttcgggttgcttatttcaatttccacaatgg 989
Db 533 AATTGTTCTATTACCAATGCGGCATCTCGGTTGCTTATTTCATTTATTCACAAATGG 474
Qy 990 gaggaggccttttgattgcacgtacgtatgtaactttcaacataaactctgttgatagtatc 1049
Db 473 GAGGAGGCGCTTTGATTGCTCAGTAGTCACATTCAACCATTAACCTCTGTGTGATAAGTATC 414
Qy 1050 cagcaaatctcgaattttaacaacttcgcgcctctcaaatgttgaccacacgaaca 1109
Db 413 CAGCAATTTCTGCAATTTTAAACAACCTTCGCGCTCTTCAAAATTTTGACCACACGCAACA 354
Qy 1110 tgacctcattccattcattgattggcttgggtggactcaactatcagatcgagcacc 1169
Db 353 TGACTCCATCTCCATTCATTGATTGGCTTTGGGGTGGACTCAATTTATCAGATCGAGCACC 294
Qy 1170 acttgttcccaacaatgcacgttgcacatctgaatgcttgctggaatattgtgaagaat 1229
Db 293 ACTGTGTCCCAACAATGCGACCTTGCAATCTGAATCTGCTTGCATGAATATGTGAAAGAAAT 234
Qy 1230 ggtgcaagagaaataatctcttaccctcgtcgatgactactttgacggatgcaatga 1289
Db 233 GGTGCAAGAGAAATATCTTCTTACCCTCGTCGATGACTACTTTGACGGATATGCAATGA 174
Qy 1290 atttgcaacaattgaaaaatattggtgagcattcaagctaaagctgcctaaacaatct 1349
Db 173 ATTTGCAACAATTGAAAAATATGGCTGAGCACATTCAGCTAAAGCTGCCTAAACAATCT 114
Qy 1350 ggggttccaaaaagtctttcttg--tttttaaatattaattcttggaaattattgttt 1407
Db 113 GGGTGTTCAAAAAGTTTTTCTGTGTTTTTTTAAATTTAATTTCTTTGAAATTAATTTGTTT 54
Qy 1408 tcgctcattcttccattcccttttctggtagaaataaaacctgtttt 1458
Db 53 FCCGTCATCTCTCCATCCCTTTTC--GGTAGAAATAAAACCTTGTTTT 4

RESULT 2
BJ139067/c
LOCUS BJ139067 746 bp mRNA linear EST 23-JAN-2002
DEFINITION BJ139067 unpublished oligo-capped cDNA library, C. elegans L1 stage
Caenorhabditis elegans cDNA clone yk1142e08 3', mRNA sequence.
ACCESSION BJ139067
VERSION BJ139067.1 GI:18299233
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
Eukaryote; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditiodea
; Rhabditiidae; Pelodierinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 746)
AUTHORS Kohara, Y., Shin-i, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.
and Sugano, S.
TITLE A complementary view of the C.elegans genome
JOURNAL Unpublished (2002)

COMMENT

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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
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Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES

Location/Qualifiers
source
1..746
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk1142e08"
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elegans L1 stage"
/sex="hermaphrodite"
/tissue_type="whole animal"
/dev_stage="L1"

BASE COUNT 233 a 139 c 156 g 218 t
ORIGIN

Query Match 50.4%; Score 736.4; DB 10; Length 746;
Best Local Similarity 99.9%; Pred. NO. 6.5e-126;
Matches 737; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 642 ccaaaaatgtaattgatcatgacgtgatctgacttggcaccacttttcgatttacc 701
Db 746 CCACAAATGTAATGATCATGACGGTGATATGCACTTGGCACCACCTTTTCGCAATTATTC 587
Qy 702 caggagattgtgcaagtataaggccagctttgaaaaagcaattctcaagattgtaccat 761
Db 686 CAGGAGATTTGTGAAGTATAAGGCAGCTTTGAAAAAGCAATTTCTCAAGATTGTACCAT 627
Qy 762 atcaactctctatttcccgcaatgcttccaatctccgtttctcatgagcgttcagt 821
Db 626 ATCAACATCTCTATTTCACCGCAATGCTTCCAATGCTCCGTTTCTCATGGAGTGGTCACT 567
Qy 822 cagttcaatgggtattcaaaagagaatcaaatggagtcacaaagctctatcaaaagaaatgcat 881
Db 566 CAGTTCAATGGGTATTCAAGAGAAATCAATGAGCTACAAAGGTCTATCAAAAGAAATGCAAT 507
Qy 882 tctgggagcaagcaacaattgttgacattgggcttgggtattctatcaaatgttcttat 941
Db 506 TCTGGAGCAAGCAACAATTTGTTGACATTTGGCTTGGGTATTCATCAATTTGTTCTTAT 447
Qy 942 taccacaatggccacttcgggttgcatttatttcaaatatttcaaatggagagagccttt 1001
Db 446 TACCAACATGGCCACTTCGGGTTGCTTATTTCATTTTCAAAAATGGAGGAGGCCCTTT 387
Qy 1002 tgattgctcacgttagtcatctttcaaccataaactctgttgataagtatccagccaattctc 1061
Db 386 TGATTGCTCACGTAGTCACATTTCAACCATAACTCTGTTGATAAGTATCCAGCAATTCCTC 327
Qy 1062 gaattttaacaacacttcgcctcttcaaatatttgaccacacgcgaacatgactccaatctc 1121
Db 326 GAAATTTAAACAACCTTCGCGCTCTTCAAAATTTTGACCACACGCAACATGACTCCATCTC 267
Qy 1122 cattcaatgattggcttgggtggagcacaattatcaaatcgagcaccacttgttcccaa 1181
Db 266 CATTCATTGATTGGCTTTGGGGTGGAGCTCAATTTATCAGATCGAGCACCACCTTTGTTCCCAA 207
Qy 1182 caatgccacgttgcattcgaatgcttgcgtgaaatatgtgaaagaaatggtgcaagaga 1241
Db 206 CAATGCCACGTTGCAATCTGAATGCTTGCATGAATATGTGAAAGAAATGGTCAAGAGA 147
Qy 1242 ataacttcttaccctcgttcgagactacttgcaggtatgcaatgcaatgttgcaacaat 1301
Db 146 ATAATCTTCTTACCTCGTCGATGACTACTTTTGACGGATATGCAATGAAATTTGCAACCAAT 87
Qy 1302 tgaataatggtcagcacattcaagctaaagctgcctaaacaactctgggtgttcaaaa 1361
Db 86 TCAAAATATGGCTGAGCACATTCAGGCTTAAAGCTTAAAGCTTAAACAATCTGGGGTGTCAAAA 27

QY 1362 agtttttttctgtttttt 1379
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Db 26 ACTTTTCTCTGTTT 9

RESULT 3
BJ129368/c
LOCUS
DEFINITION
Caenorhabditis elegans cDNA clone yk1029h10 3', mRNA sequence.
ACCESSION
BJ129368
VERSION
BJ129368.1 GI:18289525
KEYWORDS
EST.
SOURCE
Caenorhabditis elegans.
ORGANISM
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE
1 (bases 1 to 761)
AUTHORS
Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
TITLE
A complementary view of the C.elegans genome
JOURNAL
Unpublished (2002)
COMMENT
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1..761
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk1029h10"
/clone_lib="unpublished oligo-capped cDNA library, C.
elegans L1 stage"
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/tissue_type="whole animal"
/dev_stage="L1"

BASE COUNT 248 a 135 c 157 g 220 t 1 others
ORIGIN

Query Match 50.4%; Score 736.4; DB 10; Length 761;
Best Local Similarity 98.8%; Pred. No. 6.5e-126;
Matches 752; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

QY 690 tcgcatttattccaggagatttgcgaagtataaggccagctttgaaaaagcaattctca 749
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Db 761 TCGCATTTATTCAGGAGATTGTGCAAGTATAAGGCCAGCTTTGAAAAAGCAATTCTCA 702

QY 750 agattgtaccatatcaacatctctatttccacgcaatgcttccaatgctccgtttctcat 809
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Db 701 AGATTGTACCATATCAACATCTCTATTTCACCGCAATGCTTCCAATGCTCCGTTTCTCAT 642

QY 810 ggaactgggtcagtcagttcaatgggtattcaagagaaatcaaatggagatacaaggtctatc 869
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Db 641 GGACTGGTCAGTCAGTTCAATGGGTATTCAAGAGAAATCAATGGATGACAGGCTATC 582

QY 870 aaagaaatgcattctctggagcagcaacaatttggacattgggcttgggtattctatc 929
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Db 581 AAGAAGATGCATCTCGGAGCAAGCAACAATTTGTTGGACATTGGGCTGGGTATTCTATC 522

QY 930 aatttcttattaccaacatggcacttcgggttgcatttctattctatttccacaatgg 989
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Db 521 AATTGTCTTATACCAATGCCACTTCGGGTGCTTATTTCATTATTTCACAAATGG 462

QY 990 gaggaggcttttgcacagtagtcactttcaaccataactctctgttgataagtcac 1049
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Db 461 GAGGAGGCCCTTTGATGCTACGATGACACTTTCAACCATCAACTCTGTGTGATGATC 402

QY 1050 cagccaattctogaattttaacaacttcgcgcgtcttcaaattttgaccacacgcaaca 1109
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Db 401 CAGCCAAATCTCGAATTTTAAACAACACTTCGCCGCTCTTCAAATTTTGACCACACGCAACA 342

QY 1110 tgactccatctccattcattgattgggttgactccttgggtgagactcaattatcagatcgacacc 1169
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Db 341 TGACTCCATCTCCATTCAITGATGTGGCTTTGGGGTGGACTCAATTAATCATGATCGAGCACC 282

QY 1170 acttgttcccaacaatgcccacgttgcaatctgaatctgctgctgaaatattgtgaaagaat 1229
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Db 281 ACTTGTTCACCAAAATGCCACGTTGCAATCTGAATCTGTCATGAAATATGTGAAAGAAT 222

QY 1230 ggtgcaagagagaataatcttcctacctcctcgtcgtgactacttgcgcgatatgcgaatga 1289
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Db 221 GGTGCAAGAGAAATAATCTTCCTTACCTCGTCGATGACTACTTTGACGGATATGCAATGA 162

QY 1290 atttgcacaattgaaaaatatgctgagcacattcaactcaagctaaagctcctaacaatct 1349
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Db 161 ATTGCAACAATTTGAAAAATATGGCTGAGCACATTCAGCTAAAGCTGCCTAACAATCT 102

QY 1350 ggggtgtcaaaaagttttttcttg--tttttaaatatttcttcttggaaattatttgttt 1407
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Db 101 GGGGTGTCAAAAAGTTTTCITGTTTTTTTAAATTAATCTCTTGAAATATTATTGTT 42

QY 1408 tcgcattcttctccattcccttcttctggtagataaaa 1448
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Db 41 TCGGTCTCTTCTCCATTCCTCCCTTTTCGCGTAGAAAAATAAA 1

RESULT 4
BJ149952/c
LOCUS
DEFINITION
763 bp mRNA linear EST 24-JAN-2002
BJ149952 unpublished oligo-capped cDNA library, C. elegans L1 stage
Caenorhabditis elegans cDNA clone yk1280d08 3', mRNA sequence.
ACCESSION
BJ149952
VERSION
BJ149952.1 GI:18317937
KEYWORDS
EST.
SOURCE
Caenorhabditis elegans.
ORGANISM
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE
1 (bases 1 to 763)
AUTHORS
Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
TITLE
A complementary view of the C.elegans genome
JOURNAL
Unpublished (2002)
COMMENT
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1..763
/organism="Caenorhabditis elegans"
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/db_xref="taxon:6239"
/clone="yk1280d08"
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elegans L1 stage"
/sex="hermaphrodite"
/tissue_type="whole animal"
/dev_stage="L1"

BASE COUNT 249 a 135 c 159 g 220 t
ORIGIN

Query Match 50.2%; Score 733.8; DB 10; Length 763;
Best Local Similarity 99.2%; Pred. No. 2e-125;
Matches 759; Conservative 0; Mismatches 2; Indels 4; Gaps 2;

QY 690 tcgcatttattccaggagatttgcgaagtataaggccagctttgaaaaagcaattctca 749

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Db 763 TCGCATATTATTCAGGAGATTGTGCAAGTATPAAGCCAGCTTTGAAAAAGCAATCTCA 704
Qy 750 agatgtaccatatacaatctctatttcacgcgaatcttccaatgctcgtttctcat 809
Db 703 AGATTGTACCATATCAACATCTCTATTTCACGCAATGCTTCCAATGCTCGGTTTCTCAT 644
Qy 810 ggcgtggtcagtcagttcaatgggtattcaagaagaatacaaatggagtcacaggtctatc 869
Db 643 GGACTGGTCAGTCAGTTCAATGGGTATTCAAGAGAAATCAAGTGGAGTACAGGTCTATC 584
Qy 870 aaagaaatgcattctcgggagcaagcaacaatttgggacatttgggacttgggtattctatc 929
Db 583 AAAGAAATGCATCTCGGAGCAAGCAACAATTTGTTGGACATTTGGGCTTGGGTATTCTATC 524
Qy 930 aattgtcttattacaacatgcccacitcgggttgccttatttcaatttccacaaatgg 989
Db 523 AATTGTCTTATTACCAATGGCCACATTCGGGTTGCTTATTTCATTTATTCACAAATGG 464
Qy 990 gaggaggccttttgattgctcacgttagtcactttcaaccataactctgttataagtatc 1049
Db 463 GAGGAGGCTTTTGATTGCTCAGTAGTCACCTTTCAACCATTAACCTCTGTTGATAGTATC 404
Qy 1050 cagccaattctgaattttaaacaaacttcgcgcctcttcaaatcttgaccacacgcaaca 1109
Db 403 CAGCCAAATCTCGAATTTTAAACAACCTTCGCCGCTCTTCAAAATTTTGACCACGCAACA 344
Qy 1110 tgaactcattctcatttgaattggttgggttgggtgagctcaattatcagatcagagacc 1169
Db 343 TGACTCCATCTCCATCATTTGATGCTGCTTTGGGTTGGGACTCAATTTATCAGATCGAGAC 284
Qy 1170 actgttcccaacaatgcaatgctgaatctgaaatgctgctggaatattgtgaagaat 1229
Db 283 ACTGTTCCCAACAATGCCACGTTGCAATCTGAATGCTTGCATGAATATGTGAAAGAAT 224
Qy 1230 ggtcgaagagaataatcttctacgttcgtgatgactacttggacggatagcaatga 1289
Db 223 GGTGCAAGAGAAATATCTCTTACCTCGTGCATGACTTTTGACGGATATGCAATGA 164
Qy 1290 atttgcacaattgaaaaatgctgagcacattcaagctcaagctcctaaacaatct 1349
Db 163 ATTTGCACAAATGAAAAATATGGCTGAGCACAATTCAGCTTAAGCTGCCCTAAACAATCT 104
Qy 1350 ggggttccaaaagtttttcttg--tttttaaatatttaattcttggaaattattgttt 1407
Db 103 GGGTCTTCAAAAAGTTTTTCTTGTGTTTTTTTAAATTTAAATCTTTTGAAATATTATTGTT 44
Qy 1408 tccgcatcttctccatctccctttcttctgtagaataaaacct 1452
Db 43 TCCGTCATCTTCTCCCATTCCTTT--CGGTAGAAATATAAACCT 1

RESULT 5
LOCUS BJI2883/3
DEFINITION BJI28883 unpublished oligo-capped cDNA library, C. elegans L1 stage
Caenorhabditis elegans cDNA clone yk1024a12 3', mRNA sequence.
ACCESSION BJI28883
VERSION 1
KEYWORDS EST.
SOURCE BJI28883.1 GI:18289040
ORGANISM Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Pelodierinae; Caenorhabditis.
1 (bases 1 to 756)
Kohara, Y., Shin-i, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.
and Sugano, S.
A complementary view of the C.elegans genome
Unpublished (2002)
Contact: Tadasi Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
```

```
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
I. .756
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk1024a12"
/clone_lib="unpublished oligo-capped cDNA library, C. elegans L1 stage"
/sex="hermaphrodite"
/tissue_type="whole animal"
/dev_stage="L1"

BASE COUNT 248 a 135 c 157 g 216 t
ORIGIN

Query Match 50.0%; Score 731.4; DB 10; Length 756;
Best Local Similarity 99.6%; Pred. No. 5.4e-125;
Matches 744; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

Qy 689 ttcgcatttattccaggagatttgcgaagtataaaggccagctttgaaaaagcaattctc 748
Db 756 TTCGCATTTATTCCAGGAGATTGTGCAAGTATPAAGGCCAGCTTTGAAAAAGCAATCTCTC 697
Qy 749 aagattgtaccatatacaatctctatttcacgcgaatcttccaatgctcgtttctca 808
Db 696 AAGATTGTACCATATCAACATCTCTATTTCACGCAATGCTTCCAAATGCTCGGTTTCTCA 637
Qy 809 tggactgtcagtcagttcgaatgggtatttcaagagaatacaaatggagtagcaagctctat 868
Db 636 TGGACTGTGTCAGTCAGTTCAATGGGTATTCAAGAGAAATCAAAATGGAGTACAAAGTCTAT 577
Qy 869 caagaaatgcatctcgggagcaagcaacaatttgttgacattgggttgggtattctat 928
Db 576 CAAAGAAATGCAATCTTGGGAGCAAGCAACAATTTGTTGGACATTTGGGCTTGGGTATTCTAT 517
Qy 929 caattgttcttattaccaatcgccacttcgggttgccttatttatttatttcacaaatg 988
Db 516 CAATTGTTCTTATTACCAACATGCGCACTTCGGGTGCTTATTTCATTATTTCACAATG 457
Qy 989 ggaggagccttttgattgctcagtagtcaactttcaaccataactcgttggataagtat 1048
Db 456 GGAGGAGGCTTTTGATTGCTCAGCTAGCTACTTTCAACCATAACTCTGTTGATAAGTAT 397
Qy 1049 ccagccaattctgaattttaaaaaacttcgccctcttcaaattttgaccacagcaac 1108
Db 396 CCAGCCAATTTCTGAAATTTTAAACAACCTTCGCCGCTCTTCAAAATTTTGACCACAGCAAC 337
Qy 1109 atgactccatctccattcattgattgggttgggtggactcaattatcagatcgagcac 1168
Db 336 ATGACTCCATCTCCATTCATTGATTGGCTTTGGGTTGGACTCAATTTATCAGATCGAGCAC 277
Qy 1169 cacttgttcccaacaatgccagtttgcgaatgtaatgctgctgtaataatgtgaaagaa 1228
Db 276 CACTTGTTCCTCCCAACAATGCCAGTTCGAATCTGAATGCTTGCATGAAATATGTGAAAGAA 217
Qy 1229 tgggtcgaagagaataatcttcccttaccctcgtcgtcgtactcttgcggtatgcaatg 1288
Db 216 TGGTGCAAGAGAAATAATCTTCCCTTACCTCGTGGATGACTACTTTTGACGGATATGCAATG 157
Qy 1289 aatttgcacaattgaaaaatattggctgagcacattcaagcttaagcttaagcttaagcaatc 1348
Db 156 AATTGTCAACAATTCAGAAATATGGCTGAGCACATTTCAAGCTTAAGCTGCCTTAACAATC 97
Qy 1349 tgggtgttcaaaaagtttttcttg--tttttaaatatttaattcttggaaattatttgtt 1406
Db 96 TGGGTGTTCAAAAAGTTTTTCTTGTGTTTTTTTAAATTTAAATCTTCTTGAATATTATTGTT 37
Qy 1407 ttcgcatcttctccatctccctttt 1433
Db 36 TCCGTCATCTTCTCCCATTCCTTT 10
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RESULT 6
BJ128630/c 743 bp mRNA linear EST 23-JAN-2002
LOCUS BJ128630 unpublished oligo-capped cDNA library, C. elegans L1 stage
DEFINITION Caenorhabditis elegans cDNA clone yk1021a08 3', mRNA sequence.
ACCESSION BJ128630
VERSION BJ128630.1 GI:18288787
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 743)
AUTHORS Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
TITLE A complementary view of the C.elegans genome
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
FEATURES
source
1..743
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk1021a08"
/clone_lib="unpublished oligo-capped cDNA library, C.
elegans L1 stage"
/sex="hermaphrodite"
/tissue_type="whole animal"
/dev_stage="L1"
BASE COUNT 243 a 132 c 156 g 212 t
ORIGIN
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Query Match 49.8%; Score 727.4; DB 10; Length 743;
Best Local Similarity 99.6%; Pred. No. 3e-124;
Matches 740; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

Qy 690 tcgcattattccaggagatttgcgaagtataagccagctttgaaaaagaattctca 749
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Db 743 TCGCATTTATCCAGAGATTGTGCAAGTATAGCCAGCTTTGAAAGAAGCAATTCTCA 684
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Qy 750 agattgtaccatatcaacatctctatttcacgcgaatgcttccaatgctccgtttctcat 809
|||||
Db 683 AGATTGTACCATATCAACATCTCTATTTCACCGCAATGCTTCCATGCTCGTTTCTCAT 624
|||||

Qy 810 ggaatggtcagtcagttcaatgggtatttcaagaagatacaaatgaggtacaaaggctatc 869
|||||
Db 623 GGACTGGTCAGTCAGTTCAATGGGTATTCAAGAAGATCAAAATGGAGTACAAAGGCTATC 564
|||||

Qy 870 aaagaatgcatctcggagcaagaacaattgttgacattggccttggtattctatc 929
|||||
Db 563 AAGAAGATGCAATCTGGGAGCAAGCAACAATTTGTTGGACATTGGGCTGGGTATTCTATC 504
|||||

Qy 930 aattgttcttattaccaatggtccacttcggttgcttatttcattatttcacaaatgg 989
|||||
Db 503 AATTGTTCTATTACCAATGGCCATCTCGGGTTGCTATTTCATTATTTCACAAATGG 444
|||||

Qy 990 gaggaggccttttgattgtcagctagtcactttcaacataaactctgttgataagatc 1049
|||||
Db 443 GAGGAGGCGCTTTTGATTGCTACGCTAGTCACCTTCAACCATAACTCTGTTGATAAGTATC 384
|||||

Qy 1050 cagccaatctcgaatttaacaacttcgcgctcttcaaatgttgaccacacgcacaaca 1109
|||||
Db 383 CAGCCAAATTCGGAATTTAAACAACACTTCGGCGCTCTTCAAATTTTGACCACACGCAACA 324
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Qy 1110 tgactcatctccattcattgattggcttgggtgactcaattatcagatcgagcacc 1169
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Db 323 TGACTCCATCTCCATTCATTGATTGGCTTTGGGTGGACTCAATTATCAGATCGAGCACC 264
|||||

Qy 1170 acttgttcccaacaatgcacagttgcaatctgaatctgctgtaaatatgtgaaagaat 1229
|||||
Db 263 ACTTGTTCACACAATGCCAGCTTGCAATCTGAATCTTGCATGAAATATGTGAAAGAAT 204
|||||

Qy 1230 ggtgcaaaagagaataatcttcttacctcgtcgtgactacttctgacggtatgcaatga 1289
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Db 203 GGTGCNAAAGAGAATAATCTTCTTACCTGCTGATGACTACTTTTGACGGATATGCAATGA 144
|||||

Qy 1290 atttgcacaattgaaaaataatggctgagcacattcaagctcaaaagctgctaaacaatct 1349
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Db 143 ATTTGCAACAATTTGAAAAATATGGCTGAGCACATTCAAGCTAAAGCTGCCTAAACAATCT 84
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Qy 1350 ggggtgtcaaaaagtttttttcttg--tttttaaatatttaattcttgaaattattgttt 1407
|||||
Db 83 GGGTGTTCAAAAAGTTTCTTGTGTTTTTTTAAATTTAAATCTTTTGAAATATTATTGTTT 24
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Qy 1408 tcggtcattctctccattccc 1430
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Db 23 TCGGTGATCTTCTCTCCATTTCCC 1

RESULT 7
BJ129934/c 742 bp mRNA linear EST 23-JAN-2002
LOCUS BJ129934 unpublished oligo-capped cDNA library, C. elegans L1 stage
DEFINITION Caenorhabditis elegans cDNA clone yk1036d04 3', mRNA sequence.
ACCESSION BJ129934
VERSION BJ129934.1 GI:18290091
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 742)
AUTHORS Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
TITLE A complementary view of the C.elegans genome
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
FEATURES
source
1..742
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk1036d04"
/clone_lib="unpublished oligo-capped cDNA library, C.
elegans L1 stage"
/sex="hermaphrodite"
/tissue_type="whole animal"
/dev_stage="L1"
BASE COUNT 242 a 132 c 156 g 212 t
ORIGIN
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Query Match 49.6%; Score 724.8; DB 10; Length 742;
Best Local Similarity 99.5%; Pred. No. 8.9e-124;
Matches 738; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

Qy 690 tcgcattattccaggagatttgcgaagtataagccagctttgaaaaagaattctca 749
|||||
Db 742 TCGCATTTATCCAGAGATTGTGCAAGTATAGCCAGCTTTGAAAGAAGCAATTCTCA 683
|||||

Qy 750 agattgtaccatatcaacatctctatttcacgcgaatgcttccaatgctccgtttctcat 809
|||||
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Db 682 AGATTGTACCATATCAACATCTCTATTTCACGCAATCTTCCAAATGCTCGTTTCTCAT 623
Qy 810 gactgggtcagctcaattcaatgggtattcaagaagaaatcaaatggatcagaagctctatc 869
Db 622 GCATGCTGCTAGTCAATGGGTATTCAAAGAGAAATCAAAATGAGCACAAGGCTATC 563
Qy 870 aaagaaatgcatctctgggagcaagaacaattgttgacattgggctgggtggtattctatc 929
Db 562 AAAGAAATGCATCTCGGAGCAAGCAACAATTTGTGGACATTTGGCTTGGGTATTCATC 503
Qy 930 aatgttcttattaccaacataggcaacttcgggttggttctatttcaataattcaaaatgg 989
Db 502 AATGTTCTTATTACCAACATGGCCACTTCGGGTGCTTATTTATTTATTCACAAATGG 443
Qy 990 gagagggcttttgattgctcagctagtcacttcaacataaactctgttgataagatc 1049
Db 442 GAGGAGGCTTTTGNATGCTCAGCTAGTCACTTTCAACCAATCACTCTGTTGATAGTATC 383
Qy 1050 cagcaattctcgaattttaacaacttcgcgcgtctctcaaattttgaccacacgcaaca 1109
Db 382 CAGCCAATTCGAAATTTAAACAACATTCGCGCTCTTCAAAATTTTGACCACACGCAACA 323
Qy 1110 tgactccatctccattcattgattggttgggttgactcaaatattcagatcagagcacc 1169
Db 322 TGACTCCATCTCCATTCATTGATTTGGCTTTGGGTGGACTCAATATATCAGATCAGACACC 263
Qy 1170 actgttcccaacaatgcccgttgcaatctgaatgcttcgtaaaatctgaaagaat 1229
Db 262 ACTGTTCCCAACAATGCCAGCTTGCAATCTGAATGCTTGCAATGATGTAAGAAAT 203
Qy 1230 ggtgcaagagaataatctctaccctgcgtgactgactcttgacggatagatcaatga 1289
Db 202 GGTGCAAGAGAAATATCTCTTACCTCGTCTGATGACTACTTTGACGGATATGCAATGA 143
Qy 1290 atttgcaacaattgaaataatgctgagacattcaagctaaagctgcctaaacaatct 1349
Db 142 ATTTGCAACAATGAAAAATATGGCTGAGCACATTCAAAGCTTAAAGCTGCCTTAAACAATCT 83
Qy 1350 ggggttccaaaagtctttctctg--tttttaaatataatcttgaattattgttt 1407
Db 82 GGGGTCTCAAAAAGTTTTTCTGTTTTTTTTTAAATTTAAATCTTTGAAATATTTGTTT 23
Qy 1408 tccgtcattctctccattcc 1429
Db 22 TCCGTCTCTCTCTCCATTC 1
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RESULT 8

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BJ146824/c
LOCUS
DEFINITION BJ146824 unpublished oligo-capped cDNA library, C. elegans L1 stage
Caenorhabditis elegans cDNA clone yk1239a08 3', mRNA sequence.
ACCESSION BJ146824
VERSION BJ146824.1 GI:18306990
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
Kohara,Y., Shin-i., Thierri-Mieg,J., Thierri-Mieg,D., Suzuki,Y.
1 (bases 1 to 751)
and Sugano,S.
A complementary view of the C.elegans genome
Unpublished (2002)
Contact: Tadasu Shin-i
Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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FEATURES

RESULT 9
BJ134106/c

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source 1. .751
/organism="Caenorhabditis elegans"
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elegans L1 stage"
/sex="hermaphrodite"
/tissue_type="whole animal"
/dev_stage="L1"
BASE COUNT 243 a 133 c 154 g 218 t 3 others
ORIGIN
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Query Match 49.5%; Score 724.4; DB 10; Length 751;
Best Local Similarity 98.5%; Pred. No. 1.le-123;
Matches 740; Conservative 0; Mismatches 9; Indels 2; Gaps 1;
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Qy 700 tccaggagattgtgcaagtataaggccagctttgaaaaagcaattctcagagattgtacc 759
Db 751 TCCAGNAGATTGTGCAAGTATAAGGCCAGCTTTGAAAAAGCAATTCTCAAGATTGTACC 692
Qy 760 atatacaatctctatttaccgcaatgcttccaatgctccgtttctccatgagactgttca 819
Db 691 ATATCAACATCTNTATTTCACGCAATGCTTCCAAATGCTCCGTTTCTCATGGACTGGTCA 632
Qy 820 gtccagttcaatgggtattcaagagaaatcaaatggagtcacaggtctatcaaaagaaatgc 879
Db 631 GTCAGTTCAATGGGTATTCAAAGAGAAATCAAAATGGAGTACAAAGTCTATCAAGAAATGC 572
Qy 880 attcggagcaagaacaattgttgacattgggctgggtattctctatcatcaattgttctt 939
Db 571 ATTCTGGGAGCAAGCAACAATTTGTGGACATTTGGCTTGGGTATTTCTATCAATTTGTTCTT 512
Qy 940 attcacaacatggccacttcgggttctatttatttatttatttcaaaaatgggagagacct 999
Db 511 ATTACCAACATGGGCACATTCGGGTGCTTATTTCTATTTTTCACAAATTTGAGGAGGCGCT 452
Qy 1000 ttgtatgctcacgtagtcactttcaaccataactctgttgataagtatcagacaaatc 1059
Db 451 TTTGATTTGCTACGTAGTCACTTTCAACCATAACTCTGTGTGATAAGTATCCAGCAATTC 392
Qy 1060 tcgaattttaacaacttcgcgcctcttcaaatatttgaccacacgcaacatgactccatc 1119
Db 391 TCGAATTTTAAACAACATTCGCGCTCTTCAAAATTTTGACCAACACACATGACTCCATC 332
Qy 1120 tceattcattgattggctttgggttgactcaattatcagatcgagcaccactgttccc 1179
Db 331 TCCATTCTATTGTTGGCTTTGGGTGGACTCAATTTATCAGATCGAGCACCCTTTGTTCCC 272
Qy 1180 acaatgccagcttgcaatctgaaatgcttcggtgaaatattgaaagaatggtgcaaga 1239
Db 271 AACAAATGCCAGTTGCAATCTGAATGCTTGCATGAATATGTGAAAGAAATGCTGCAAGA 212
Qy 1240 gaataattctcttaccctcgtcgtgactactcttgacggatattgacggaatgcaattgcaaca 1299
Db 211 GAATAAATCTTCTTACCTCGTCGATGACTACTTTGACGGATATGCAATGAATTTGCAACA 152
Qy 1300 attgaaaaataatggctgagcaattcaagctaaagctgcctaaacaatctgggtgttcaa 1359
Db 151 ATTGAAAAATATGGCTGAGCACATTCAGCTTAAAGCTGCCTTAAACAATCTCGGGTGTCAA 92
Qy 1360 aaagtctttctctg--tttttaaatataatcttctgaaatatttcttccgtcattc 1417
Db 91 AAAGTTTTTCTTCTTTTTTTTAAATTTAAATCTTTGAAATTTATTTGTTTTCGGTCATTC 32
Qy 1418 ttccctcattccctttcttctggtagaaataaa 1448
Db 31 TTCTCCATTCCTCTTTCGGTGTAGAAAAATAA 1
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LOCUS      BJ134106      748 bp      mRNA      linear      EST 23-JAN-2002
DEFINITION BJ134106 unpublished oligo-capped cDNA library, C. elegans L1 stage
ACCESSION  BJ134106
VERSION    BJ134106.1 GI:18294263
KEYWORDS   EST.
SOURCE     Caenorhabditis elegans.
ORGANISM   Caenorhabditis elegans.
REFERENCE  1 (bases 1 to 748)
AUTHORS    Kohara,Y., Shin-I., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
TITLE      A complementary view of the C.elegans genome
JOURNAL    Unpublished (2002)
COMMENT    Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
            Location/Qualifiers
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            /organism="Caenorhabditis elegans"
            /strain="N2"
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            /clone="yk1084g01"
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            /tissue_type="whole animal"
            /dev_stage="L1"

BASE COUNT 244 a 134 c 156 g 214 t
ORIGIN

Query Match 49.5%; Score 724.2; DB 10; Length 748;
Best Local Similarity 99.3%; Pred. No. 1.1e-123;
Matches 738; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

Qy 697 tattccaggagattgtgcagtagataagccagctttgaaagcaattctcaagattgt 756
Db 748 TATTCAGGAGATTTGTCAAGTAGTAAGGCCAGCTTTGAAAAGCAATTCACAGATTGT 689

Qy 757 accatatcaacatctctattcacgcgaatgtctccaatgtccttctctcatgactgg 816
Db 688 ACCATATCAACATCTCTATTACCGCAATGCTTCCAATGCTCCGTTTCTCATGGACTGG 629

Qy 817 tcagtcagttcaatgggtattcaagagaatacaaatggagtacaaggtctatcaagaaa 876
Db 628 TCAGTCAGTTCAATGGGTATTCAAGAGCAATCAATGCGAGTACAGGCTATCAAGAAA 569

Qy 877 tgcattctgggagcaagcaaatgttggacattgggctgggtattctatcaattgtt 936
Db 568 TGCATTCTGGGAGCAAGCAAAATTTGTGACATTGGGCTTGGGTATTCTATCAATTGTT 509

Qy 937 ctattaccacatggccacttcgggtgtctatttctatttcaaaaatggagagg 996
Db 508 CTTATACCAATGCGGCACCTTCGGGTGTCTATTTCATTATTTCACAAATGGGAGGAGG 449

Qy 997 ccttttgattgtcacgtagtcactttcaaacataactctgttgataagttccagccaa 1056
Db 448 CCTTTTGATTGCTCAGGTAGTCACTTTCAACCATAACTCTGTTGATAGTATCCAGCCAA 389

Qy 1057 ttctcgaatttaacaacttcgcgcgtcttcaaatatttgaccacacacgaactgcc 1116
Db 388 TTCGGAATTTAAACAACCTTCGGCGCTCTTCAAAATTTTGACCACACGCAACATGACTCC 329

Qy 1117 atctccattcattatgtgctttggggtggactcaattatcagatcgagaccacttgtt 1176
Db 328 ATCTCATTCATTGATTGGCTTTGGGGTGGACTCAATTTATCAGATCGAGCACCACTTGT 269

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Qy 1177 cccacaatgccacgttcaacttgaatgcttgcgtgaaatgtgaaagaatggtgcaa 1236
Db 268 CCCACAATGCCACGCTGCAATCTGAATGCTTGCATGAATATGCAAGAATGTTGCAA 209

Qy 1237 agagaataatcttcttacctcgatgactactcttggacggatgataatgaattgca 1296
Db 208 AGAGAATAATCTTCCTTACCTCGTGCATGACTACTTGTGACGGATATGCAATGAATTCGA 149

Qy 1297 acaattgaaaaatatggctgagcacatcaactcaagctgaagctgctaaacaatctgggtgt 1356
Db 148 ACAATTGAAAATATGGCTGAGCACATTCACGCTAAGCTGCCTAAACAATCTGGGTGTT 89

Qy 1357 caaaaagtgttttcttctg--tttttaaatttaattcttcttgaattattgtttcccgta 1414
Db 88 CAAAAGTGTTCCTGTTGTTTTTTTAAATTTAAATCTTTGAAATATTATTTGTTTCCGTC 29

Qy 1415 ttctctccatccctcttctctg 1437
Db 28 TTCTTCTCCCATTCCTCTTTTCGG 6

RESULT 10
BJ148511/c
LOCUS      BJ148511      750 bp      mRNA      linear      EST 24-JAN-2002
DEFINITION BJ148511 unpublished oligo-capped cDNA library, C. elegans L1 stage
ACCESSION  BJ148511
VERSION    BJ148511.1 GI:18316496
KEYWORDS   EST.
SOURCE     Caenorhabditis elegans.
ORGANISM   Caenorhabditis elegans.
REFERENCE  1 (bases 1 to 750)
AUTHORS    Kohara,Y., Shin-I., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
            and Sugano,S.
TITLE      A complementary view of the C.elegans genome
JOURNAL    Unpublished (2002)
COMMENT    Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
            Location/Qualifiers
            1..750
            /organism="Caenorhabditis elegans"
            /strain="N2"
            /db_xref="taxon:6239"
            /clone="yk1263h03"
            /clone_lib="unpublished oligo-capped cDNA library, C.
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            /sex="hermaphrodite"
            /tissue_type="whole animal"
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BASE COUNT 244 a 134 c 156 g 216 t
ORIGIN

Query Match 49.4%; Score 722.2; DB 10; Length 750;
Best Local Similarity 99.3%; Pred. No. 2.7e-123;
Matches 736; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

Qy 699 ttccaggagattgtgcagtagataagccagctttgaaagcaattctcaagattgtac 758
Db 750 TTCCAGGAGATTTGTGCAAGTAGTAAGGCCAGCTTTGAAAAGCAATTCCTCAAGATTGTAC 691

Qy 759 catatcaacatctctatttcaccgcaatgcttccaatgctcgttctctcatgactggtc 818
Db 690 CATATCAACATCTCTATTTCACCGCAATGCTTCCCAATGCTCCGTTTCTCATGACTGGTC 631

Qy 819 agtcagttcaatgggtatttcaagagagaatcaaatggagtacaaggtctctatcaagaaatg 878

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Db 630 AGTCAGTTCAATGGGTATTTCAAAGAGATCAAAATGGAGTACAAGTCTATCAAGAAATG 571
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Db 570 CATTCGGGAGACACAAATGTTGGACATGGGCTTGGGTATCTATCAATGTCT 511
Qy 939 tattaccaaatgagccacttgggtgttcttatttcatttccaaatggagagagcc 998
Db 510 TATTTACCAACATGGCCACTTGGGTGCTTATTTTCAATTTTCAAAATGGAGAGGCC 451
Qy 999 ttttgattgcacgtatgcatttcaaccataactctgttgataagtatccagccaatt 1058
Db 450 TTTTGATTGCTCAGCTAGTCACTTTCAACCATTAACCTCGGTGATAAGTATCCAGCCAAAT 391
Qy 1059 ctggaattttaaaacacttcgctctcttcaaattttgaccacacgcacatgactccat 1118
Db 390 CTCGAAATTTAAACAACTTCGCCGCTCTTCAAAATTTGACCACACGCAACATGACTCCAT 331
Qy 1119 ctccattcatgattggcttgggtggactcaaatatcagatcgagcaccacttgttcc 1178
Db 330 CTCCAATTCATTGATTGGCTTTGGGTGGACCTCAATATATCAGATCGAGCACCACCTGTGTC 271
Qy 1179 caacaatgccagttgcaatctgaatgcttgcgtgaaatatgtgaaagaaatgggtgcaag 1238
Db 270 CAACAATGCCAGCTGGCAATCTGAATGCTTCATGAAATATGTGAAGAAATGGTGCAAG 211
Qy 1239 agaatcaatcttccctacctctgcgatgactacttggcggtatgcaatgaatttgcaac 1298
Db 210 AGAATAATCTTCCCTACCTCGTGCATGACTACTTTGACGGATATGCAATGAATTTGCANAC 151
Qy 1299 aattgaaaaatatggctgagcacattcaagctaaagctgcctaaacatctgggtgttca 1358
Db 150 AATTGAAAAATATGGCTGAGCACATTCAGCTAAAGCTGCCTAAACAATCTGGGTGTCA 91
Qy 1359 aaagttttttcttg--ttttttaaatttaattcttggaaattattgttttcogtcaat 1416
Db 90 AAAAGTTTTTCTGTGTTTTTAAATTAATCTTTGAAATATTATTTGTTTCGCTCAAT 31
Qy 1417 ctctccctccatccctttctg 1437
Db 30 CTCTCTCCATTCCTTTTCGG 10

RESULT 11
BJ128407/c
LOCUS
DEFINITION BJ128407 762 bp mRNA linear EST 23-JAN-2002
Caenorhabditis elegans cDNA clone yk1018d12 3', mRNA sequence.
VERSION BJ128407.1 GI:18288564
KEYWORDS EST.
SOURCE BJ128407
ORGANISM Caenorhabditis elegans.
REFERENCE 1 (bases 1 to 762)
AUTHORS Kohara,Y., Shin-I., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
TITLE A complementary view of the C.elegans genome
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-I
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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Best Local Similarity 99.0%; Pred. No. 8e-123;
Matches 756; Conservative 0; Mismatches 4; Indels 4; Gaps 3;
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Db 702 AGATTTTACCATATCAACATCTCTATTTTCAACGCAATGCTTCCAATGCTCCGTTTCTCAT 643
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Db 642 GGACTGGTCACTCAGTTCATGGGTATTTCAAGAGAAATCAATGGAGTACAGGTCTATC 583
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Db 462 GAGGAGGGCTTTTGTATGCTCAGCTAGTCACTTTCAACCAATAACTCTCTTGATAGTATC 403
Qy 1050 cagcgaattctcggaattttaaacaaacttcgcgctcttcaaattttgaccacacgcaaca 1109
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ACCESSION BJ149141


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ORGANISM Caenorhabditis elegans.
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REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
AUTHORS ; Rhabditidae; Peloderinae; Caenorhabditis.
          1 (bases 1 to 731)
          Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
          and Sugano,S.
TITLE A complementary view of the C.elegans genome
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
          National Institute of Genetics
          1111 Yata, Mishima, Shizuoka 411-8540, Japan
          Tel: 81-559-81-6856
          Fax: 81-559-81-6855
          Email: tshini@genes.nig.ac.jp.
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Matches 722; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

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VERSION AU210015.1 GI:14846014
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ORGANISM Caenorhabditis elegans.
          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
          ; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 720)
AUTHORS Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
          and Sugano,S.
TITLE A complementary view of the C.elegans genome
JOURNAL Unpublished (2001)
COMMENT Contact: Yuji Kohara
          Genome Biology Lab.
          National Institute of Genetics
          Yata 1111, Mishima, Shizuoka 411, Japan
          Tel: 81-559-81-6854
          Fax: 81-559-81-6855
          Email: ykohara@lab.nig.ac.jp.
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Db 1	1 C 1			

TITLE and Sugano, S.
JOURNAL A complementary view of the C. elegans genome
COMMENT Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES Location/Qualifiers
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/clone_lib="unpublished oligo-capped cDNA library, C.
elegans L1 stage"
/sex="hermaphrodite"
/tissue_type="whole animal"
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BASE COUNT 235 a 131 c 149 g 210 t
ORIGIN

Query Match 48.0%; Score 701.8; DB 10; Length 725;
Best Local Similarity 98.9%; Pred. No. 1.5e-119;
Matches 717; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

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Db 725 ATTCCAGGAGATTGTCAGATATAAGCCAGCTTTGAAAAAGCAATTCCTCAAGATTGTA 666
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Qy 818 cagtcagttcaatgggtattcaagagagaatcaaatggagtgctctatacaagaaat 877
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Qy 878 gcattctgggaggaagaacaattgttgacattggcgttggttattctatcaaatgttc 937
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Search completed: August 7, 2002, 02:08:49
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 6, 2002, 16:21:46 ; Search time 31.23 Seconds
(without alignments)
2453.947 Million cell updates/sec

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
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 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
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 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phase:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	600.5	24.9	419	10	Q9SWQ9 euglena gra
5	592	24.6	520	10	Q9LEMG ceratodon p
6	590.5	24.5	525	10	Q9ZNM2 physcomitre
7	577	23.9	459	10	Q944W4 pythium irr
8	569.5	23.6	467	3	Q96VC3 mucor circi
9	559	23.2	483	10	Q9LENO ceratodon p
10	557	23.1	457	3	Q9UVV3 mortierella
11	556	23.1	457	3	Q9UVV3 mortierella
12	549	22.8	457	3	Q9HEV4 mortierella
13	546	22.7	457	3	Q9HEV1 mortierella
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29	406	16.8	444	4	O60427 homo sapien
30	406	16.8	444	4	O96T10 homo sapien
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ALIGNMENTS

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DT 01-DEC-2001 (TREMREL. 19, Last annotation update)
DE DELTA6-FATTY-ACID-DESATURASE.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97268723; PubMed=9108131;
RA Savanova O., Smith M.A., Lapinskas P., Stobart A.K., Dobson G.,
Christie W.W., Shewry P.R., Napier J.A.;
"Expression of a borage desaturase cDNA containing an N-terminal
cytochrome b5 domain results in the accumulation of high levels of
delta6-desaturated fatty acids in transgenic tobacco.";
Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98149727; PubMed=9480865;
RA Napier J.A., Hey S.J., Lacey D.J., Shewry P.R.;
"Identification of a caenorhabditis elegans Delta6-fatty-acid-
desaturase by heterologous expression in saccharomyces cerevisiae.";
Biochem. J. 330:611-614(1998).
RL EMBL: AF031477; AACI5586.1;
DR InterPro: IPR001199; Cyt_B5.
DR InterPro: PS000566; Lipocln_cytFABP.
DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
DR PROSITE: PS00213; LIPOCALIN; UNKNOWN_1.
SQ SEQUENCE 443 AA; 51740 MW; 9513CA7C5A7E9A06 CRC64;

April 97

Query Match 100.0%; Score 2410; DB 5; Length 443;
Best Local Similarity 100.0%; Pred. No. 1.9e-194;
Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MVDKNASGLRMKVDGKWLKYLSEELVKKHGGAVIEQYRNSDATHIFHAFHEGSSQAYKQ 60
Db 1 MVDKNASGLRMKVDGKWLKYLSEELVKKHGGAVIEQYRNSDATHIFHAFHEGSSQAYKQ 60
Qy 61 LDLLKKHGEHDEFLEKQLEKRLDKVDINVSAYDVSVAQEKMKWSEFEKLRQKLDHDDGLMK 120
Db 61 LDLLKKHGEHDEFLEKQLEKRLDKVDINVSAYDVSVAQEKMKWSEFEKLRQKLDHDDGLMK 120
Qy 121 ANETYFLFKALSTLSIMAFAYLOYLWYITSACLLALAWOQFGLWTHFCHQOQPTKNRP 180
Db 121 ANETYFLFKALSTLSIMAFAYLOYLWYITSACLLALAWOQFGLWTHFCHQOQPTKNRP 180
Qy 181 LNDTISLFFGNFLOGFSRDWKKHNTHTHAATNVIDHDGDDIDLAPLFAFIPGDLCKYKAS 240
Db 181 LNDTISLFFGNFLOGFSRDWKKHNTHTHAATNVIDHDGDDIDLAPLFAFIPGDLCKYKAS 240
Qy 241 FEKAILKIVPYQHLYFTTAMLPMLRFSWTGQSVQWVFKEQNMKEYKYORNAFWEQATIVGH 300
Db 241 FEKAILKIVPYQHLYFTTAMLPMLRFSWTGQSVQWVFKEQNMKEYKYORNAFWEQATIVGH 300
Qy 301 WAWFYQLFLLPTWPLRVAYFIISOMGGGLLIAHVVTFNHNSVDKYKEMCKENNLPLYLVDY 420
Db 301 WAWFYQLFLLPTWPLRVAYFIISOMGGGLLIAHVVTFNHNSVDKYKEMCKENNLPLYLVDY 420
Qy 361 ILTTRNMTSPFIDWLGGLNYQIEHHLFPTMPRCNLNACVYKWKEMCKENNLPLYLVDY 420
Db 361 ILTTRNMTSPFIDWLGGLNYQIEHHLFPTMPRCNLNACVYKWKEMCKENNLPLYLVDY 420
Qy 421 FDGYAMNLQQLKNAEHIQAKAA 443
Db 421 FDGYAMNLQQLKNAEHIQAKAA 443
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RESULT 2
Q23221 ID Q23221 PRELIMINARY; PRT; 443 AA.
-AC Q23221;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE W08D2.4 PROTEIN.
GN W08D2.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Swinburne J., Ainscough R.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-99069613; PubMed-9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL: Z70271; CAA94233.2; -.
DR InterPro: IPR001199; Cyt_B5.
DR InterPro: IPR000566; Lipocin_cytFABP.
DR PROSITE: PS02055; CYTOCHROME_B5_2; 1.
DR PROSITE: PS00213; LIPOCALIN; UNKNOWN_1.
SQ SEQUENCE 443 AA; 51772 MW; 9513D611ECB99A06 CRC64;
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Query Match 99.98; Score 2407; DB 5; Length 443;
Best Local Similarity 99.88; Pred. No. 3.4e-194;
Matches 442; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MVDKNASGLRMKVDGKWLKYLSEELVKKHGGAVIEQYRNSDATHIFHAFHEGSSQAYKQ 60
Db 1 MVDKNASGLRMKVDGKWLKYLSEELVKKHGGAVIEQYRNSDATHIFHAFHEGSSQAYKQ 60
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Qy 61 LDLLKKHGEHDEFLEKQLEKRLDKVDINVSAYDVSVAQEKMKWSEFEKLRQKLDHDDGLMK 120
Db 61 LDLLKKHGEHDEFLEKQLEKRLDKVDINVSAYDVSVAQEKMKWSEFEKLRQKLDHDDGLMK 120
Qy 121 ANETYFLFKALSTLSIMAFAYLOYLWYITSACLLALAWOQFGLWTHFCHQOQPTKNRP 180
Db 121 ANETYFLFKALSTLSIMAFAYLOYLWYITSACLLALAWOQFGLWTHFCHQOQPTKNRP 180
Qy 181 LNDTISLFFGNFLOGFSRDWKKHNTHTHAATNVIDHDGDDIDLAPLFAFIPGDLCKYKAS 240
Db 181 LNDTISLFFGNFLOGFSRDWKKHNTHTHAATNVIDHDGDDIDLAPLFAFIPGDLCKYKAS 240
Qy 241 FEKAILKIVPYQHLYFTTAMLPMLRFSWTGQSVQWVFKEQNMKEYKYORNAFWEQATIVGH 300
Db 241 FEKAILKIVPYQHLYFTTAMLPMLRFSWTGQSVQWVFKEQNMKEYKYORNAFWEQATIVGH 300
Qy 301 WAWFYQLFLLPTWPLRVAYFIISOMGGGLLIAHVVTFNHNSVDKYKEMCKENNLPLYLVDY 420
Db 301 WAWFYQLFLLPTWPLRVAYFIISOMGGGLLIAHVVTFNHNSVDKYKEMCKENNLPLYLVDY 420
Qy 361 ILTTRNMTSPFIDWLGGLNYQIEHHLFPTMPRCNLNACVYKWKEMCKENNLPLYLVDY 420
Db 361 ILTTRNMTSPFIDWLGGLNYQIEHHLFPTMPRCNLNACVYKWKEMCKENNLPLYLVDY 420
Qy 421 FDGYAMNLQQLKNAEHIQAKAA 443
Db 421 FDGYAMNLQQLKNAEHIQAKAA 443
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RESULT 3
Q9XTB7 ID Q9XTB7 PRELIMINARY; PRT; 447 AA.
-AC Q9XTB7;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-MAY-1999 (TReMBLrel. 12, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE DELTA5-FATTY ACID DESATURASE.
GN FAT-4 OR DES-5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99117288; PubMed-9917342;
RA Watts J.L., Browse J.;
RT "Isolation and characterisation of a delta5-fatty acid desaturase from
RT Caenorhabditis elegans."
RL Arch. Biochem. Biophys. 362:175-182(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-99059458; PubMed-9845325;
RA Michaelson L.V., Napier J.A., Lewis M., Griffiths G., Lazarus C.M.,
RA Stobart A.K.;
RT "Functional identification of a fatty acid delta5 desaturase gene from
RT Caenorhabditis elegans."
RL FEBS Lett. 439:215-218(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Swinburne J.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE-99069613; PubMed-9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL: AF114440; AAD13294.1; -.
DR EMBL: AF078796; AAC95143.1; -.
DR EMBL: Z81122; CAB61031.1; -.
SQ SEQUENCE 447 AA; 52348 MW; D7E09CE0E2975015 CRC64;
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Db 206 KTLINVSIVATSIATIIISLYKSYRA-VLSASLMLGLFIQCGWLSHDFLHQVFETRIND 264
Qy 184 TISLFFNGFQGGSRDWMKDKHNTHHAATNVIDH-----DGDIDLAPLEAFIPGDLCKYK 238
Db 265 VGVVGNVVLGFSVSNWKTHNLUHAAPNECDQKYPIDEDIDTLPIIWSKDLLATVE 324
Qy 239 ASFEKAILKIVPYQHLVFTAMLPMLRFSWTQSQSVQWVEK-ENQMEYKYVYORNAFWEQATI 297
Db 325 S---KTLMLRVLYQHLFELVLLTPARASWLFWSAAFTLRPELTIGEXLLER-----GTM 375
Qy 298 VGHWAM-----VFYQLFLLPTWPLRVAYFIISOMGGGLLIAHVVTNNHNSVDKYPANRIL 353
Db 376 ALHYIWFNSVAFY---LLPGWK-PVVMVVSSELMGSLGVLGYVFLSHNGMEVYNTS---- 427
Qy 354 NNFAALOILTRNMTSPFPFDLWGLGNYOIEHHLFPTMPRCNLNACVKYKWKCKENNL 413
Db 428 KDFYNAQIATRODIKAGVNDWFTGGNROIEHHLFPTMPRNLNKNKISPHVETLCKRKHGL 487
Qy 414 PYLVDDYFDGYAMNLOOLKNMAE---HIQAKAA 443
Db 488 VYEDVSMASGYRVLYKTLKOVADAASHQOLAAS 520

RESULT 6
Q92NW2 ID Q92NW2 PRELIMINARY; PRT; 525 AA.
AC Q92NW2;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-OCT-2001 (Tremblrel. 18, Last annotation update)
DE DELTAG-ACYL-LIPID DESATURASE.
GN DES6.
OS Physcomitrella patens (Moss).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Funariaceae; Funariales; Funariaceae; Physcomitrella.
OX NCBI_TaxID=3218;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HEDW. B. S. G.;
RX MEDLINE=98416756; Pubmed=9744093;
RA Girke J., Schmidt H., Zaehnering U., Reski R., Heinz E.;
RT "Identification of a novel delta 6-acyl-group desaturase by targeted
RT gene disruption in Physcomitrella patens.";
RC Plant J. 15:39-48(1998).
CL -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AJ222981; CAAL1033.1; -
DR EMBL; AJ222980; CAAL1032.1; -
DR HSSP; P04166; IB5M.
DR InterPro; IPR001199; Cyt_B5.
DR Pfam; PF001173; heme_1; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 525 AA; 59369 MW; 530F158B0C97C83F CRC64;
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Query Match 24.5%; Score 590.5; DB 10; Length 525;
Best Local Similarity 32.5%; Pred. No. 2.6e-41;
Matches 140; Conservative 76; Mismatches 160; Indels 55; Gaps 12; -

Qy 19 LYLSEELVKHPGGAVIEQYRNSDATHIFHAFHEGSSQAYKQDLKLLKHGHDLEKQL 78
Db 127 YVDVSNFADEHPGGSVISTYFGRDGTDFVSSFFHAATWKILQ-----DFYIGDV 175
Qy 79 EKRLDKVDINVSAYDVSAQEKKVESFEKLQKLDHDDGLMKANETVFLPKAISTLSIMA 138
Db 176 ER-----VEPTPELKKDFREMRALFLREQLFKSKLIYVMKLLTNVAL-- 218
Qy 139 FAFYLYQLVIGW-----YITSACLLALAAWQFGWLTHFEFCHQOQTKNRPNDTISLFFGNE 192
Db 219 FAASATIAICWSKTTISAVLASACMAALCFQCGWLSHDFLHNQVFETRNLNEVGVVIGNA 278
Qy 193 LQGSRDWKKDKHNTHHAATNVIDH-----DGDIDLAPLEAFIPGDLCKYKASFEKAILK 247
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Db 279 VLGFSTGWMKEKLNHLHAAPNECDQYQPIDEIDITLPLIWSKDILATVE---NKTFLR 335
Qy 248 IVPYQHLVFTAMLPMLRFSWTQSQSVQWVEKQYVYORNAFWEQATIVGHWAM-VFY 306
Db 336 ILQYQHLFFNGLLFFARGSWLFW--WRYTSTAVLSPV---DRLLEKGTVLVHFVFWGT 390
Qy 307 QLFLLLPTW-PLRVAYFIISOMGGGLLIAHVVTNNHNSVDKYPANRILNFAALQILTR 365
Db 391 ACYLLPGWKPL--VWMAVTELMGMLLGFVFLSHNGMEVYNS--KEFVSAQIVSTR 444
Qy 366 NMTSPPIDMLWGLNLYOIEHHLFPTMPRCNLNACVKYKWKCKENNLPLYLVDDYFDGYA 425
Db 445 DIKGINFNDWFTGGNROIEHHLFPTMPRNLNKNKIAPIRVEFCKHGLVEDVSIATGTC 504
Qy 426 MNLQOLKNMAE 436
Db 505 KVLKALKEVAE 515

RESULT 7
Q944W4 ID Q944W4 PRELIMINARY; PRT; 459 AA.
AC Q944W4;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE DELTA-6 FATTY ACID DESATURASE.
OS Pythium irregulare.
OC Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae; Pythium.
OX NCBI_TaxID=36331;
RN [1]
RP SEQUENCE FROM N.A.
RA Hong H., Datta N., Mackenzie S.L., Qiu X.;
RT "A delta-6 fatty acid desaturase from Pythium irregulare.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF419296; AALI3310.1; -
SQ SEQUENCE 459 AA; 52498 MW; 286464DA761BE055 CRC64;
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Query Match 23.9%; Score 577; DB 10; Length 459;
Best Local Similarity 33.9%; Pred. No. 2.9e-40;
Matches 147; Conservative 67; Mismatches 158; Indels 62; Gaps 16;

Qy 17 KWLVLSEELVKHPGGAVIEQYRNSDATHIFHAFHEGSSQAYKQDLKLLKH--GEHDEFL 74
Db 39 KW-----DSHPGGSVMLTQAGEDATDAFAVHPSSA-----LKLEQFYVGDVDETS 85
Qy 75 EKQLEKRLDKVDINVSAYDVSAQEKKM---VESFEKLQKLDHDDGLMKANETVFLPKAI 131
Db 86 KAEIE-----GEPASDEERARRERINEFIASRYRLRVKVMGMDLYDASALYAWKL 137
Qy 132 STLSTI---MAFAFYLOYLWYITSACLLALAWOQFGWLTHFEFCHQOQTKNRPNDTISL 187
Db 138 STFGIIVLSMAICFFNFNSFAMVYVAGVIMGLFYQOQSWLAHDFLHNQVCNRTLGNLIGC 197
Qy 188 FFGNFLAGSRDWMKDKHNTHHAATNVIDH-----DGDIDLAPLEAFIPGDLCKYK 238
Db 198 LVGNAGQGSVQWKKKHNHLHHAHPNL--HSAKDEGFIGDPDIDTMTPLAWSKE---MAR 252
Qy 239 ASFEKA--ILKIVPYQHLVFTAMLPMLRFSWTQSQSVQWVEKQYVYORNAF--WEQ 294
Db 253 KAFESAHPGFIRNOAFLYPFLLL-LARLSWAQSFYFVTE--FSFGIFDKVDFDGPKEK 309
Qy 295 ATIVGHWAM-----VFYQLFLLPTWPLRVAYFIISOMGGGLLIAHVVTNNHNSVDKYPAN 349
Db 310 AGLVHIWQIAIPIFCNMSLFE-----GVAYFLMGQACGLLLALVFSIGHNGSVYERE 365
Qy 350 SRLNNFAALQILTRNMTSPFPIDWLWGLGNYOIEHHLFPTMPRCNLNACVKYKWKCK 409
Db 366 TK--PDFWOLQVTTTRNIRASVFMDFWTGGNLYQIDHHLFPLVPRHNLKPVNVLKLSICK 423
Qy 410 ENNLPLYLVDDYFDG 423
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Db 424 EFDIPFHETGFEG 437
|::|::|::|::|

RESULT 8
Q96VC3 PRELIMINARY; PRT; 467 AA.
AC Q96VC3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DELTA-6 FATTY ACID DESATURASE.
GN D6D.
OS Mucor circinelloides.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
OC Mucor.
OX NCBI_TaxID=36080;
RN [1]
RP SEQUENCE FROM N.A.
RA Michinaka Y., Aki T., Murashima C., Shimauchi T., Nakajima T.,
RA Kawamoto S., Shigeta S., Ono K., Suzuki O.;
RT "Cloning and characterization of a delta-6 fatty acid desaturase from
RT Mucor circinelloides."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB052086; BAB69055.1; -.
SQ SEQUENCE 467 AA; 53387 MW; 8162163D3CB5C591 CRC64;

Query Match 23.68; Score 569.5; DB 3; Length 467;
Best Local Similarity 32.78; Pred. No. 1.3e-39;
Matches 152; Conservative 69; Mismatches 191; Indels 53; Gaps 15;
Qy 2 VVDKNASGRMKVGVKWLSEELVKKHPGG-AVIEQYRNSDATHIFHAFHEGSSQAYKQ 60
Db 25 VLDKKPEARLIVENKVYDITDFVDPHPCGERVLLTQEGDADTVHEMPPS--AY-- 80
Qy 61 LDLLKKGHEHDFLEKLEKRL-----DKVDINVSADVSAQEKKVVESPEKLRQKLDH 115
Db 81 -ELLANCYVGD-----CEPKLPIDSTDKKALNSAAF-----AQE-----TRDLRDKLEK 123
Qy 116 DGLMKANETVFLKAI STLSTMAFAFYLYQLGW-----YITSACLLALAWQFGWLTH 168
Db 124 QGYFDASTGTFYIKVSTLLVCIVGLAI-LKAWGRESTLAVFIASLVGLFWQCGWLAH 182
Qy 169 EFCHQOQTKNRPLNDTISLFFGNFLOGFSRDWKKDKHNTHTHAATNVIDHDGIDILAPLF- 227
Db 183 DYAHYQVQIKDPNVNLFVTFGNLVQGSLSWKKKNTHTASTNVSGEDPDIDTAPILL 242
Qy 228 -----AFIPGDLCKYKASPEKAILK-IVPYQHLYFTAMLPMLRFSWTGQSVQVWFRENQ 280
Db 243 WDEFAVANFYGSLKDNASGDFRTAEHLPTQTRYFFILGFARTSWAIQSIYFSKNET 302
Qy 281 MEYKVIQORNAPFEQATVGHAWVYQIQLFLLPTWPLRV-----AYFISQMGGLLIAHV 336
Db 303 LNKs--KLLSWCERIFLIVHWFFTYCTI---AWISSIRNIAMFFVVSQITGYLLAIVF 357
Qy 337 TFHNSVDKYPANSRIINLFAALQILTRNMTSPFIDWLMGGLNYQIEHHLFTPTMPCRN 396
Db 358 AMNHGMPVYSPEANHTFEVQLQICIGROVNCIVFGDWMGLNGGLNYQIEHHLFPMPRH 417
Qy 397 LNACVKYKWKCKENNLPLYVDDYFDGYAMNLOQLKNAEHIQAK 441
Db 418 LSKVKSMVKPIAQYNIPY-HDTTVIGTIEVLQTLDFVQKISQK 461

RESULT 9
Q9LENO PRELIMINARY; PRT; 483 AA.
AC Q9LENO;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DELTA 6-FATTY ACETYLENASE.

OS Ceratodon purpureus (Moss).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Dicranidae; Dicranales; Ditrichaceae; Ceratodon.
OX NCBI_TaxID=3225;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WT3; TISSUE=PROTONEMATA;
RX MEDLINE=20307617; PubMed=10848999;
RA Sperling P., Lee M., Girke T., Zaehring U., Stymne S., Heinz E.;
RT "A bifunctional delta 6-fatty acyl acetylenase/desaturase from the
RT moss Ceratodon purpureus. A new member of the cytochrome b5
RT superfamily";
RL Eur. J. Biochem. 267:3801-3811(2000).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AJ250734; CAB94992.1; -.
DR HSSP; P04166; 1B5M.
DR InterPro; IPR001199; Cyt_B5.
DR Pfam; PF00173; heme_1; 1.
DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 483 AA; 54857 MW; C451D042169AB1C2 CRC64;
Query Match 23.28; Score 559; DB 10; Length 483;
Best Local Similarity 32.68; Pred. No. 1e-38;
Matches 136; Conservative 66; Mismatches 155; Indels 60; Gaps 13;
Qy 18 WLYLSEEL-----VKKHPGGAVIEQYRNSDATHIFHAFHEGSSQAYKOLDLLKKHGEHD 71
Db 78 WMIKVKYVDISRTADDDHPGGTVISTYFGRDGTDFATFHPPA--AWQL-----ND 127
Qy 72 EFL-EKQLEKRLKVDINVSADVSAQEKKVVESPEKLRQKLDHDDGLMKANETVFLFK- 129
Db 128 YYIGDLAREEPLD-----ELLKDYRDMRAEFVREGLFKSKKAWFLQOT 170
Qy 130 ----AISTLSMAFAFYLYQLGWYIT-SACLLALAWQFGWLTHFCHQOQTKNRPLNDT 184
Db 171 LINAALFAASTATICYDKSY--WAIVLSASLGMFLVQCGWLAHDFLHQVFNENTANSF 228
Qy 185 ISLFFGNFLOGFSRDWKKDKHNTHTHAATNVIDH-----DGDIDILAPLFAIPGDLCKYKA 239
Db 229 FGYLEGNCVGLGFSVSWRTKKNHHTAPEDEQVTPDEIDITLPIANSKEILATVES 288
Qy 240 SFEKAILKIVPYQHLYFTAMLPMLRFSWTGQSVQVWFKENQMEYKVIQORNAPFEQATIVG 299
Db 289 ---KRILRVLYQYQWIMLPFLFMARYSWTFGSLFTFNPDLSTTK-----GLIEKGTVAF 340
Qy 300 HWAWVYQOLF-LLPTWPLRVAYFIISOMGGGLLIAHVTFHNSVDKYPANSRIINLNF 358
Db 341 HYAWFSWAAPHILPGVAKPLAMVATELVAGLLLGFTLSHGKVEYNES----KDFVR 396
Qy 359 LOILTRNMTSPFIDWLMGGLNYQIEHHLFTPTMPCRNACVKYKWKCKENNLPLY 415
Db 397 AOVIITRNKRGWDFWTGGLDTQIEHHLFTPTMPCRNHYPKIAQVEALCKKHGLE 453
RESULT 10
Q9UVV3 PRELIMINARY; PRT; 457 AA.
AC Q9UVV3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DELTA-6 FATTY ACID DESATURASE.
OS Mortierella alpina.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mortierellaceae;
OC Mortierella.
OX NCBI_TaxID=64518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC32221;
RX MEDLINE=99406036; PubMed=10478922;
RA Huang Y.S., Chaudhary S., Thurmond J.M., Bobik E.G. Jr., Yuan L.,

RA Chan G.M., Kirchner S.J., Mukerji P., Knutzen D.S.;
RT *Cloning of delta12- and delta6-desaturases from Mortierella alpina
RT and recombinant production of gamma-linolenic acid in Saccharomyces
RT cerevisiae*;
RL Lipids 34:649-659(1999).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL: AF110510; AAF08685.1; -.
DR HSSP: P04166; 1B5M.
DR InterPro: IPR001199; Cyt_B5.
DR Pfam: PF00173; heme_1.1.
DR PROSITE: PS00191; CYTOCHROME_B5_1; UNKNOWN_1.
DR PROSITE: PS0255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 457 AA; 51837 MW; D90169E86911450A CRC64;

Query Match 23.1%; Score 557; DB 3; Length 457;
Best Local Similarity 32.1%; Pred. No. 1.4e-38;
Matches 143; Conservative 64; Mismatches 187; Indels 52; Gaps 11;

QY 12 MKVDGKWLXSEELVKKHGGAVIEQYRNSDATHIFHAFHEGSSQAYKQLDLLKKHGEHD 71
DB 34 MIDNK-VYDREVPDPHGGSVILTHVGKDGTDVDFTHPEAAW----- 77
QY 72 EFLEKQLEKRLDKVDINVSAYDVSVAQEKKVESFEKLRQLKLDHDDGLMKANETVFLFKAI 131
DB 78 ETLANFVVGIDESDRDIKNDDFA-AEVKRLRTLQSL-----GYDSSKAYIAFKVS 129
QY 132 STLSIMAFAYLOYLW-----YITSACLLALAWQFCGLWTFHFCQQOPTKNRPLNDT 184
DB 130 FNLCINGLSTVI-VAKWGQSTLANVLSAALLGLFWQCGWLAHDFLHHQVFDQRFWGD 188
QY 185 ISLFFGFLGSRDWWKRNTHHAATNVHDHGDIDLAPL-----FAFIG-D 233
DB 130 FNLCINGLSTVI-VAKWGQSTLANVLSAALLGLFWQCGWLAHDFLHHQVFDQRFWGD 188
QY 185 ISLFFGFLGSRDWWKRNTHHAATNVHDHGDIDLAPL-----FAFIG-D 233
DB 189 FGAFGLGVCQGFSSWKKRNTHHAAPNVHGEDPDIDTHPLTWSHALEMFSVDPDEE 248
QY 185 ISLFFGFLGSRDWWKRNTHHAATNVHDHGDIDLAPL-----FAFIG-D 233
DB 189 FGAFGLGVCQGFSSWKKRNTHHAAPNVHGEDPDIDTHPLTWSHALEMFSVDPDEE 248
QY 234 LCKYKASFEKAILKIVPYOHLFTAMLPMLRFSWGTGQVQVMEKQMEYKVVQR--NAF 291
DB 189 FGAFGLGVCQGFSSWKKRNTHHAAPNVHGEDPDIDTHPLTWSHALEMFSVDPDEE 248
QY 234 LCKYKASFEKAILKIVPYOHLFTAMLPMLRFSWGTGQVQVMEKQMEYKVVQR--NAF 291
DB 249 LTRMWSRF-----MVLNQTWTFPILSFARLSQCLSIPLVNGQAHKPSGARVPISL 302
QY 292 WEQATIVGHNAWVYQFLFPLTPPLR-VAYFIISQMGGLLIARHVTFNHNSVDKYPANS 350
DB 303 VEQLSLAHHTWVLTATMFLFKDPVNMVFLVLSQVAVCGNLLAIVFSLNHGMPVISKEE 362
QY 351 RIILNFAALQILTRNNTPSPFFIDWLGGLNYQIEHLLFPTMPCRNLCNACVKYKCKE 410
DB 363 AVDMDFTKQIIGRVDVHGLFANWFTGGLNYQIEHLLFSPMRHNFPSKIQPAVETLCKK 422
QY 411 NNLPLYVDYDFGAYMNLQOLKNAE 436
DB 423 YNRYHTTGMIEGTAEVFSRLNEVSK 448

RESULT 11
Q9UYV3 ID Q9UYV3 PRELIMINARY; PRT; 457 AA.
AC Q9UYV3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DELTA-6 FATTY ACID DESATURASE.
OS Mortierella alpina.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mortierellaceae;
OC Mortierella
OX NCBI_TaxID=64518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-IS-4;
RX MEDLINE-20035749; PubMed=10570972;
RA Sakuradani E., Kobayashi M., Shimizu S.;
RT "Delta 6-Fatty acid desaturase from an arachidonic acid-producing
RT Mortierella fungus. Gene cloning and its heterologous expression in a
RT fungus, Aspergillus.*;

RL Gene 238:445-453(1999).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL: AB020032; BAA85588.1; -.
DR HSSP: P04166; 1B5M.
DR InterPro: IPR001199; Cyt_B5.
DR Pfam: PF00173; heme_1.1.
DR PROSITE: PS00191; CYTOCHROME_B5_1; UNKNOWN_1.
DR PROSITE: PS0255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 457 AA; 51816 MW; 5C4B3D7312439543 CRC64;

Query Match 23.1%; Score 556; DB 3; Length 457;
Best Local Similarity 31.8%; Pred. No. 1.7e-38;
Matches 142; Conservative 64; Mismatches 188; Indels 52; Gaps 11;

QY 12 MKVDGKWLXSEELVKKHGGAVIEQYRNSDATHIFHAFHEGSSQAYKQLDLLKKHGEHD 71
DB 34 MIDNK-VYDREVPDPHGGSVILTHVGKDGTDVDFTHPEAAW----- 77
QY 72 EFLEKQLEKRLDKVDINVSAYDVSVAQEKKVESFEKLRQLKLDHDDGLMKANETVFLFKAI 131
DB 78 ETLANFVVGIDESDRDIKNDDFA-AEVKRLRTLQSL-----GYDSSKAYIAFKVS 129
QY 132 STLSIMAFAYLOYLW-----YITSACLLALAWQFCGLWTFHFCQQOPTKNRPLNDT 184
DB 130 FNLCINGLSTVI-VAKWGQSTLANVLSAALLGLFWQCGWLAHDFLHHQVFDQRFWGD 188
QY 185 ISLFFGFLGSRDWWKRNTHHAATNVHDHGDIDLAPL-----FAFIG-D 233
DB 189 FGAFGLGVCQGFSSWKKRNTHHAAPNVHGEDPDIDTHPLTWSHALEMFSVDPDEE 248
QY 234 LCKYKASFEKAILKIVPYOHLFTAMLPMLRFSWGTGQVQVMEKQMEYKVVQR--NAF 291
DB 249 LTRMWSRF-----MVLNQTWTFPILSFARLSQCLSIPLVNGQAHKPSGARVPISL 302
QY 292 WEQATIVGHNAWVYQFLFPLTPPLR-VAYFIISQMGGLLIARHVTFNHNSVDKYPANS 350
DB 303 VEQLSLAHHTWVLTATMFLFKDPVNMVFLVLSQVAVCGNLLAIVFSLNHGMPVISKEE 362
QY 351 RIILNFAALQILTRNNTPSPFFIDWLGGLNYQIEHLLFPTMPCRNLCNACVKYKCKE 410
DB 363 AVDMDFTKQIIGRVDVHGLFANWFTGGLNYQIEHLLFSPMRHNFPSKIQPAVETLCKK 422
QY 411 NNLPLYVDYDFGAYMNLQOLKNAE 436
DB 423 YNRYHTTGMIEGTAEVFSRLNEVSK 448

RESULT 12
Q9HEY4 ID Q9HEY4 PRELIMINARY; PRT; 457 AA.
AC Q9HEY4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DELTA6-FATTY ACID DESATURASE.
OS Mortierella isabellina.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mortierellaceae;
OC Mortierella
OX NCBI_TaxID=91625;
RN [1]
RP SEQUENCE FROM N.A.
RA Ming-Chun L., Li L., Guo-Wu H., Li Z., Lai-Jun X.;
RT "Cloning and sequencing analysis of delta6-fatty acid desaturase gene
RT from Mortierella isabellina.*;
RL Junwu Xitong 0:0-0(2001).
DR EMBL: AF306634; AAG38104.1; -.
DR HSSP: P04166; 1B5M.
DR InterPro: IPR001199; Cyt_B5.
DR PROSITE: PS00191; CYTOCHROME_B5_1; UNKNOWN_1.
DR PROSITE: PS0255; CYTOCHROME_B5_2; 1.
SQ SEQUENCE 457 AA; 51772 MW; 868E7EB21172D5AF CRC64;

	Query Match Best Local Similarity 22.8%; Score 549; DB 3; Length 457; Matches 142; Conservative 63; Mismatches 189; Indels 52; Gaps 11;	
QY	12 MKVDGKWLYLEELVKKHGGCAVIEIQYNRSDATHTFHAFHSGSSOAYQLDLLKKHGHEHD 71 : : : : : : : : : : : : : : : : :	
Dd	34 MIIDNK-VYDVREVPDPHGVGSVLTHVGKGDTGFDFTFHPFAAM-----77 : : : : : : : : : : : : : : : : :	
QY	72 EFLEKOLEKRDLKDVIDINVSADSVSAQAOKMVESFEKLROKLDDGLMKANETYFLPKAI 131 : : : : : : : : : : : : : : : : :	
Dd	78 ETLANFYGDIDESDRAIKNDDEA-AEVRKLTLFOSL-----GYDSSKAYYAPKVS 129 : : : : : : : : : : : : : : : : :	
QY	132 STLSIMAFAYLYOLGW-----YTISACLLALAWQQFGWLTETFCHQPTKNRPLNMT 184 : : : : : : : : : : : : : : : : :	
Dd	130 FNLCITIGLSITEI-VAKWGTSTLANLVISAALLGLFWQCWGMLAHDFLHHQVFQRWFMDL 188 : : : : : : : : : : : : : : : : :	
QY	185 ISLPFNGFLOGFSROWMWDKINTHAATNTVIDDHOGDIDLAPL-----FAFIGP-D 233 : : : : : : : : : : : : : : : : :	
Dd	189 FGAFLGVCGCFGSSWKDKINTHAAPNVNHGEDPDIDTPLLTWSEHALEMFDSDPDEE 248 : : : : : : : : : : : : : : : : :	
QY	234 LCKYKASFEKAILXIVPYQHLYFTAMLPMFRSQTGSQVMFKENQMKEYVIYQR--NAF 291 : : : : : : : : : : : : : : : : :	
Dd	249 LTRWSRF-----MYLNQWTWEYPILLSFARSLWCLOSILVLNPNGOAHKPSGARVISL 302 : : : : : : : : : : : : : : : : :	
QY	292 WEQATIYGHWNAVRYQLFLTTPBLR-YAYFIISOMGGGLLIAHVVTPNHNNSVDKYSPANS 350 : : : : : : : : : : : : : : : : :	
Dd	303 VEQLSLAAHMWTYLATWFLFKDPPNMVMYFLVSQAVCGNELLAIVFSLNHNMGMPVISKEE 362 : : : : : : : : : : : : : : : : :	
QY	351 RILNFAALQILTIRNMTGPSFIDNLGCLNYQEHLHFPTMPRCNLNACYKVYEKCCE 410 : : : : : : : : : : : : : : : : :	
Dd	363 AVDMDFTKIIITGRDVHGPLGANFTGGLNYQEHLHFPSMPRHNFSKIOPAVETLCKK 422 : : : : : : : : : : : : : : : : :	
QY	411 NNLPLYLDVDDYDGAMNLQCLKMAAE 436 : : : : : : : : : : : : : : : : :	
Dd	423 YGVRYHTTGMEGTAEVFSRLNEYSK 448 : : : : : : : : : : : : : : : : :	
RESULT	13	
Q9HEY1	ID O9HEY1 PRELIMINARY; PRT; 457 AA.	
OC	O9HEY1	
DI	01-MAR-2001 (TrEMBLrel. 16, Created)	
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)	
DT	01-DEC-2001 (TrEMBrel. 19, Last annotation update)	
DS	DELTA 6-FATTY ACID DESATURASE.	
OE	Mortierella alpina.	
OC	Eukaryota: Fungi; Zygomycota; Zygomycetes; Mucorales; Mortierellaceae;	
OC	Mortierella.	
OX	NCBI_Taxid=64518;	
RN	[1]	
RN	SEQUENCE FROM N.A.	
RA	Xing L., Li M., Liu L., Hu G., Zhang L.;	
RP	"Expression of Mortierella alpina delta 6-fatty acid desaturase gene	
RT	in Saccharomyces cerevisiae." ;	
RL	Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases .	
DR	EMBL; AF307940; AAG45092.1; -,	
DR	HSSP; P04166; IBSM.	
DR	InterPro: IPR001199; Cyt.B5.	
DR	PROSITE; PS00191; CYTOCHROME_B5_1; UNKNOWN_1.	
DR	PROSITE; PSS0255; CYTOCHROME_B5_2; 1.	
SQ	SEQUENCE 457 aa; 51885 MW; 4B0ACODD15D19DA1 CRC64;	

```
Query Match      22.7% ; Score 546; DB 3; Length 457;
Best Local Similarity 32.4%; Pred. No. 1.2e-37;
Matches 144; Conservative 62; Mismatches 189; Indels 50; Gaps 11;
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Qy	72	EFLKLEKRLDKVDINVSAYDVSVAQEKKMWSEFEKLROKLHDDGLMKANETFFLPKAI	131
Dy	72	: : : : : : : : : : : : : : : :	
Db	78	ETLANFYVGDDIDESDRATIKND DFA-AEVRKLRITLFQSL-----GYDSSKAYYAFKVS	129
Qy	132	STLSIMAF A-FYLOVLGWYIT-----SACLLALAWOQFGWLTHFCHOOPTKNRPLNDTI	185
Dy	132	: : : : : : : : : : : : : : : :	
Db	130	FNLCLWGLUSTIVAKRGOTSTLANELSAALLGLFWOQRGNLAHLFHVOVQDFRWGDLF	189
Qy	186	SLFNGFNLFQGSRDWKDHKHNTHAAATNVIDHDGDIDLAPL-----FAFIG-DL	234
Dy	186		
Db	190	GAFLGDCQCGFSSSWKDKHNTHAAPNVHGCDPDIDTFLPLLTHSEHALEMFSVDPEEL	249
Qy	235	CKYRASPFKAALKIVPYQHLLFTAMLPMLESWTGSCSQVOWFKENOMEYKVQOR--NAFW	292
Dy	235	: : : : : : : : : : : : : : : :	
Db	250	TRMWSRF-----MYLNQTWFYFILSFARLSQCILFLVPNGQAHPKSGARKVPISLV	303
Qy	293	EOATIVGHAMWVEQLFPLTPWPLR-VAYFIISOMGGILLIAHVVTFNHNSVDKYPANSR	351
Dy	293	: : : : : : : : : : : : : : : :	
Db	304	EQLSLAMHTWYLATMFELFDKPVMNMYFIVSQAVCNLLAIYFSLNHNGMPVISKEEA	363
Qy	352	ILNFPAALQILTRNTMTSPFIDMLWGGLNYQIEHHLLFPTPRCNLNACVKYKWECKEN	411
Dy	352	: : : : : : : : : : : : : : : :	
Db	364	VDMDFETKIITGRDVHPGLFANNFTGLNYQIEHHLLFPSPMRHFNFSKIQA VETLCKKY	423
Qy	412	NLPYLVDYFCGYAMNLOOLKNMAE	436
Dy	412	: : : : : : : : : : : : : : : :	
Db	424	GVRYYHTGMIECTAEVFSRLNEVSK	448
RESULT	14		
ID	Q9HDF4	PRELIMINARY;	PRT; 357 AA.
AC	Q9HDF4;		
DT	01-MAR-2001	(TrEMBLrel. 16, Created)	
DT	01-MAR-2001	(TrEMBLrel. 16, Last sequence update)	
DT	01-DEC-2001	(TrEMBLrel. 19, Last annotation update)	
DE	DELTA 6-FATTY ACID DESATURASE (FRAGMENT).		
OS	Mortierella alpina.		
OC	Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mortierellaceae;		
OX	Mortierella.		
NCBI_TaxId	64518;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Xing L., Li M., Liu L., Hu G., Zhang L.;		
RT	"Cloning and sequence analysis of the conserved region of delta 6-		
RT	fatty acid desaturase gene from Mortierella alpina."		
RL	Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.		
RL	Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Xing L., Li M., Liu L., Hu G., Zhang L.;		
RT	"Cloning and sequence analysis of the conserved region of delta 6-		
RT	fatty acid desaturase gene from Mortierella alpina."		
RL	Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; AF307942; AAG45094.1; -.		
DR	EMBL; AF307941; AAG45093.1; -.		
DR	HSSP; P04166; 1B5M.		
DR	InterPro; IPR001199; Cyt B5.		
DR	PROSITE; PS00191; CYTOCHROME_B5_1; UNKNOWN_1.		
DR	PROSITE; PS50255; CYTOCHROME_B5_2; 1.		
FT	NON_TER	1	
FT	NON_TER	357	
SQ	SEQUENCE	357 AA; 40796 MW; C8D9CE1283BB16B8 CRC64;	
Query Match		20.48; Score 490.5; DB 3; Length 357;	
Best Local Similarity		33.2%; Pred. No. 3.9e-33;	
Matches 128; Conservative		50; Mismatches 158; Indels 49; Gaps 10;	
Qy	26	VKKHPGGAVIEOYRNSDATHIFAHFEGSSQAYKQLDLLKKHGEHDFPLEKLEKRLDKV	85
Dy	2	VDPHPGGSVILTHGVKGCTGCVDFTFHPAAW-----ETLANFYVGDDIES	46
Qy	86	DINVSAYDVSVAQEKKMWSEFEKLROKLHDDGLMKANETFFLPKAI STLSIMAF A-FYLO	144

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 6, 2002, 16:18:46 ; Search time 20.87 Seconds
(without alignments)
2039.654 Million cell updates/sec

Title: US-09-555-093-2
Perfect score: 2410
Sequence: 1 MYVDKNASGLRMKVDGKWL.....YAMNLOQLKNMAEHQAKAA 443

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	2382	98.8	473	1 T26280	linoleoyl-CoA desaturase
2	1092.5	45.3	447	1 T43319	Delta5 fatty acid
3	1079	44.8	454	2 H88791	protein Tl3f2.1 li
4	463.5	19.2	449	2 A84900	hypothetical prote
5	460.5	19.1	458	2 S68358	Delta8 sphingolip
6	443.5	18.4	449	2 T50555	delta-8 sphingolip
7	433	18.0	449	2 T47950	delta-8 sphingolip
8	421	17.5	523	2 JC7556	linoleoyl-CoA desaturase
9	393.5	16.3	444	2 Tl3155	linoleoyl-CoA desaturase
10	389.5	16.2	444	2 JG0180	Delta6 fatty acid
11	296.5	12.3	345	2 T36617	probable Delta6 fatty acid
12	225	9.3	368	2 S54809	linoleoyl-CoA desaturase
13	215.5	8.9	359	2 S35157	Delta6 fatty acid
14	174.5	7.2	443	2 T08136	probable omega-6 d
15	165.5	6.9	448	2 D85362	hypothetical prote
16	158.5	6.6	447	2 S53309	n-6 fatty acid desaturase
17	157.5	6.5	350	2 S43772	phosphatidylcholin
18	157.5	6.5	350	2 AH2005	phosphatidylcholin
19	148	6.1	424	2 T07742	omega-6 desaturase
20	147.5	6.1	424	2 JC5891	omega 6 desaturase
21	147	6.1	382	2 T15042	omega-6 fatty acid
22	146	6.0	352	2 B69901	fatty-acid desaturase
23	141.5	5.9	351	2 S11519	phosphatidylcholin
24	140	5.8	287	2 T11959	fatty-acid desaturase
25	138	5.7	349	2 S43770	phosphatidylcholin
26	136	5.6	347	2 S43771	phosphatidylcholin
27	133	5.5	370	2 B83034	conserved hypothet
28	130	5.4	383	2 T10480	Delta12 fatty acid
29	123	5.1	385	2 T09880	omega-6 desaturase

ALIGNMENTS

RESULT 1

T26280
linoleoyl-CoA desaturase (EC 1.14.99.25) W08D2.4 - Caenorhabditis elegans
N:Alternate names: Delta6 fatty acid desaturase
C:Species: Caenorhabditis elegans
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
C:Accession: T26280; T37238
R:Swinburne, J.; Ainscough, R.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z20188
A:Accession: T26280
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-473 <WIL>
A:Cross-references: EMBL:Z70271; PIDN:CAA94233.1; GSPDB:GN00022; CESP:W08D2.4
A:Experimental source: clone W08D2
R:Napier, J.A.; Hey, S.J.; Lacey, D.J.; Shewry, P.R.
Biochem. J. 330, 611-614, 1998
A:Title: Identification of a caenorhabditis elegans Delta6-fatty-acid-desaturase by h
A:Reference number: Z21637; M01D:98149727
A:Accession: T37238
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-38,69-430,'V',432-473 <NAP>
A:Cross-references: EMBL:AF031477; NID:g3088519; PIDN:AAC15586.1; PID:g3088520
C:Genetics:
A:Gene: CESP:W08D2.4
A:Map position: 4
A:Introns: 13/3; 39/2; 234/3; 277/3; 378/1; 413/3
C:Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase
C:Keywords: alternative splicing; oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 98.8%; Score 2382; DB 1; Length 473;
Best Local Similarity 93.4%; Pred. No. 1.3e-182;
Matches 442; Conservative 1; Mismatches 0; Indels 30; Gaps 1;

Qy 1 MVVDKNASGLRMKVDGKWLSEELVKKHGPGGAVTEQ----- 37
Db 1 MVVDKNASGLRMKVDGKWLSEELVKKHGPGGAVTEQSIPPLNKNIEIRGITTRGSSN 60
Qy 38 -----YRNSDATHIFHAFHEGSSQAYKQLDLKKHGHDEFELEKLEKLDKVDINVS 90
Db 61 ALDILYFRNSDATHIFHAFHEGSSQAYKQLDLKKHGHDEFELEKLEKLDKVDINVS 120
Qy 91 AYDVSVAQEKKMKVESFEKLROKLDHDDGLMKANETVFLFKASTLSIMAFAYLQYLGWYI 150
Db 121 AYDVSVAQEKKMKVESFEKLROKLDHDDGLMKANETVFLFKASTLSIMAFAYLQYLGWYI 180
Qy 151 TSACLLALAWQOFGWLTIEFCHQOQTKNRPLNDTISLFFGNFLOGFSRDWKKDKINTHHA 210
Db 181 TSACLLALAWQOFGWLTIEFCHQOQTKNRPLNDTISLFFGNFLOGFSRDWKKDKINTHHA 240

Db 329 YLILSFGFNLHRLSFAYLATCKNY-----RTRTLELVGITFFVFWFGSLLSLTPTWNI 382
Qy 317 RVAVFLISOMGGGLLIAHV-VTFNH--NSVDKVPANSRLNNFAALOILTRNNTPSPF 372
Db 393 RIAYIMVSIMLTFFD--HVQITLSHFGSTEDRGDPE-----PPAKMLRTTMDVDCPEW 435
Qy 373 IDLWGGGNYQIEHLLFPTMPRCNLNACVKYKWKCKENNLNLYLVDDYFDGYAMNLOQLK 432
Db 436 HDWFHGGYQYQAVHLLFPLRHLRNLRCQVPLVKKFCDEVLGHYYMYNFTSGNGVVLSTLK 495
Qy 433 NNAEHI 438
Db 496 SVADQV 501

RESULT 9
Tl3155
linoleoyl-CoA desaturase (EC 1.14.99.25) [validated] - human
N:Alternate names: Delta6 fatty acid desaturase; protein DKFp586C201.1
C:Species: Homo sapiens (man)
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jun-2000
C:Accession: Tl3155; T08765
R:Cho, H.P.; Nakamura, M.F.; Clarke, S.D.
J. Biol. Chem. 274, 471-477, 1999
A:Title: Cloning, expression, and nutritional regulation of the mammalian Delta-6 desaturase
A:Reference number: Z17612; MUID:99085046
A:Accession: Tl3155
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-444 <CHO>
A:Cross-references: EMBL:AF126799; NID:g4406527; PID:g4406528; PIDN:AAD20018.1
R:Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, March 1999
A:Reference number: Z16471
A:Accession: T08765
A:Molecule type: mRNA
A:Residues: 'RTRG', 138-428, 'D', 430, 'M', 432-444 <WAM>
A:Cross-references: EMBL:AL050118
A:Experimental source: adult uterus; clone DKFp586C201
C:Genetics:
A:Gene: GDB:FADSD6
A:Cross-references: GDB:9956652
A:Note: DKFp586C201.1
C:Superfamily: cytochrome b5 core homology
C:Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase; unsaturated fatty
F:18-94/Domain: cytochrome b5 core homology <CB5>
F:53,76/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 16.3%; Score 393.5; DB 2; Length 444;
Best Local Similarity 27.8%; Pred. No. 1.1e-23;
Matches 120; Conservative 61; Mismatches 166; Indels 85; Gaps 17;
Qy 17 KWLYLSEELV-----KHGG-AVIEQYRNSDATHIFHAFHEGSSQAYKOLDLLKKHGE 69
Db 35 RNLVIDRKVYNTKWSIQHPGQGRVIGHYAGEDATDAFRAHP-----DL----- 79
Qy 70 HDEFLEKLEKLDKVDINVSAYDSVAQEKKNVESFEKLRQKLDHDDGLMKRANETYFLFK 129
Db 80 --EFVGKEL-RPLLGLLAPEEPSQDHCKNSKITEDFDALRKRTAEDMNLKFTNHVFLLL 136
Qy 130 AISTLSIMAFAYLQYL---GWYIT--SACLLALAWQOFGWLTHEFCQQPTKNRPLNDT 184
Db 137 LAHIIALESIAFWTFYFGNGWIPTLITAFVLATSOAAGWLQHDYGHLSYRKPKWNL 196
Qy 185 ISLFGFNLOGFSRDWKKDKNTHAATNVIDHGDIDLAPLFAFIPGDLCKYKASFKA 244
Db 197 VHKFVIGHLGKASANNWNRHFQHHAKNPFIHKDPDVNN--LHVFVLGEW--QPIEYCKK 252
Qy 245 ILKIVPY--QHLTYTAMLPMLRFSWVGQVWFKEKQMEYKVYORNAFWEQATIVGH-- 300
Db 253 KLKYLPNHNOHEYFLIGPPLLIIPM-----YFOYQIIM-----TMIVHKN 292

Qy 301 -----WAWFYQLFLLPTWPLRVAYFIISQMGGLLIAHVTF-----NHNSV 343
Db 293 WYDLAWAVSYIRFITIYPF---YGIL----GALLFLNFIRFLESHWFVWVQTNHIVM 345
Qy 344 DKYPANSRLNNFAALQILTTNNMTSPSPIDWLMGGLNYQIEHLLFPTMPRCNLNACVKY 403
Db 346 E---IDQEAIRDFWSQLTATCNVEQSFNDWFSGLHNFQIEHLLFPTMPRNLHKAIDL 402
Qy 404 VKEMCKENNLPLY 415
Db 403 VKSLCAKHGIEY 414
RESULT 10
JG0180
Delta6 fatty acid desaturase (EC 1.14.99.-) [imported] - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 21-Jul-2000
C:Accession: JG0180
R:Aki, T.; Shimada, Y.; Inagaki, K.; Higashimoto, H.; Kawamoto, S.; Shigeta, S.; Ono, Biochem. Biophys. Res. Commun. 255, 575-579, 1999
A:Title: Molecular cloning and functional characterization of rat delta-6 fatty acid
A:Reference number: JG0180; MUID:99160394
A:Accession: JG0180
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-444 <AKT>
A:Cross-references: DDBJ:AB021980; NID:g4514721; PIDN:BAA75496.1; PID:g4514722
C:Superfamily: cytochrome b5 core homology
C:Keywords: heme; iron; metalloprotein; oxidoreductase; unsaturated fatty acid biosyn
F:18-94/Domain: cytochrome b5 core homology <CB5>
F:53,76/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 16.2%; Score 389.5; DB 2; Length 444;
Best Local Similarity 28.1%; Pred. No. 2.4e-23;
Matches 123; Conservative 60; Mismatches 158; Indels 97; Gaps 19;
Qy 17 KWLYLSEELV-----KKHPGG-AVIEQYRNSDATHIFHAFHEGSSQAYKOLDLLKKHGE 69
Db 35 RNLVIDRKVYNTKWSQRHPGGRVIGHYSGEDATDAFRAH-----LDLDFVGK---- 84
Qy 70 HDEFLEKQL-----EKRLDKVDINVSAYDSVAQEKKNVESFEKLRQKLDHDDGLMKAN 122
Db 85 ---FLKPLLIGELAPEEPSLDR-----GKSSQITEDFRALKKTAEDMNLKFTN 129
Qy 123 EYTFLEKAI STL SIMAFA--FYQLY--GWY--ITSACLLALAWQOFGWLTHEFCQQPT 176
Db 130 HLFF-FLLSHIIVMESIAWFI LSYFGNGWIPTVITAFVLATSOAAGWLQHDYGHLSVY 188
Qy 177 KNRPLNDITSLFNGFLOGFSRDWKKDKNTHAATNVIDHGDIDLAPLFAFIPGDLCK 236
Db 189 KKSINWNIHVHKFVIGHLGKASANNWNRHFQHHAKNPFIHKDPDI--KSLHVFVLGEW-- 244
Qy 237 KYASEKAILKIVPY--QHLTYTAMLPMLRFSWVGQVWFKEKQMEYKVYORNAFWMQ 294
Db 245 QPLEYGGKKLKLPLYNHNOHEYFLIGPPLLIIP-----MYFOYQIIMTMRRRDWDL 296
Qy 295 ATIVGHWAWVFYQL-----FLLPTWPLRVAYFIISQMGGLLIAHVVT 337
Db 297 ANAISYARFFTYTIPFYGILGALVFLNFIRFLESHW-----FVWVTQMN-----HIVM 345
Qy 338 FHNHSDVKYPANSRLNNFAALQILTRNNMTSPPIDWLMGGLNYQIEHLLFPTMPRCNL 397
Db 346 --EIDLHY-----RDWFSQLAATCNVEQSFNDWFSGLHNFQIEHLLFPTMPRNL 396
Qy 398 NACVKYKWKCKENNLPLY 415
Db 397 HKIAPLVKSLCAKHGIEY 414
RESULT 11

T36617

probable Delta6 fatty acid desaturase (EC 1.14.99.-) SCH35.42c [similarity] - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Jun-2000

C:Accession: T36617

R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, June 1999

A:Reference number: 221610

A:Accession: T36617

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-345 <OLI>

A:Cross-references: EMBL:AL078610; PIDN:CAB44385.1; GSPDB:GN00070; SCOREDB:SCH35.42c

A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: SCOEDB: SCH35.42c

C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 12.3%; Score 296.5; DB 2; Length 345;

Best Local Similarity 27.1%; Pred. No. 4.6e-16;

Matches 92; Conservative 54; Mismatches 156; Indels 37; Gaps 10;

Qy 106 FEKLRLKLDGLMKANETYPFLRAISTLSMA---FAFYQLYLGWY-ITSACLLALAWQ 161

Db 17 FARLSKKVADAGLLGRPGYYTLRTITAVTGLYAAGWAFVLVGASWMTLATAAF LAVMYG 76

Qy 162 QFGWLTHEFCHQOPTKPNPLNDTISLFGNFGFSRDWKKDKHNTHTHAATNVIDHGDGI 221

Db 77 QVALVAHMAHQVRRRRRASELSGRAGASI-GMSVGWODKTRHHAANTEDLOPDI 135

Qy 222 -----DLAPLFAFIPGDLCKYKASFKAILKIPVQHLVFTAMLPMLRFSWTSQSV 272

Db 136 GPDLLWSPDQARAATGLPRLIGRWQA-----FLFF---PLLTLE--GFNL 176

Qy 273 QWVKENOMEYKYVQRNAFWQATVGHAWVFQFLPLTPWPLRVAYFIISQMGGLLI 332

Db 177 H-VASGRAMANRRUKRRAL-DCALLAHCAVYLTAFELWPLPPGMAIAFLAVHQCLFGYVL 234

Qy 333 AHVTFENHSVDKYVPANSRILNNAALQILTRNNTPSPFDLWGLNGLYOIEHHLRPTM 392

Db 235 GSAPAPNHKGWPILTADDR--PDFLRQVLTSRNVNGGLFTDLALGGLNHQIEHHLRPSM 292

Qy 393 PRCLNLACVYKWKEMCKENNPYPYLVDDYFDGYAMNLOQL 431

Db 293 PSPNLKARAIYRRYCRDLGVDYAEATGLVASYRLALTSL 331

RESULT 12

S54809

linoleoyl-CoA desaturase (EC 1.14.99.25) - Spirulina platensis

N:Alternate names: Delta6-desaturase

C:Species: Spirulina platensis

C:Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jun-2000

C:Accession: S54809

R:Tasaka, Y.

submitted to the EMBL Data Library, May 1995

A:Reference number: S54809

A:Accession: S54809

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-368 <TAS>

A:Cross-references: EMBL:X87094; NID:g809109; PIDN:CAA60573.1; PID:g809110

C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 9.3%; Score 225; DB 2; Length 368;

Best Local Similarity 27.2%; Pred. No. 2.6e-10;

Matches 76; Conservative 46; Mismatches 111; Indels 46; Gaps 14;

Qy 191 NFIGFSRD-----WKKDKHNT-HHAATNVIDHGDIDLAPLFAFTPGD-LCKYKASF 241

Db 103 NYLSGLTHDAIGVSSYLWKFRHNVLHHTYTNILGHDEIH-----GDELVRMSPSM 153

Qy 242 EKAILKIVPYQHLVFTAMLPMLRFSWTSQSVQ-WVFKENOMEYKYVQRNAFW-EOATVIG 299

Db 154 EYRWYH--RYQHWFIFWVPIPYWSTADVTMLFKROYHDHEI--PSPTWVDIATLLA 209

Qy 300 HWAUVFQFLPLTPWPLRVAYFIISQMGG-----LLIAHVVFTHNSVDK 345

Db 210 FKAFGVAVFLII--PIAVGYSPLAEVIGASIVYVMTHTGLVACVVFMLAHVIE-PAEFLD- 264

Qy 346 YPANSRILNNAALQILTRNMT-PSPIDMLWGLNGLYOIEHHLFPTMPCNLNACVKYV 404

Db 265 -PDLHIDDEWAIQAQVTKTVDFAPNPILINNYVGLNVTQVTHHLFPHCHIHYPKIAPI 323

Qy 405 KEMCKENNPYLIV-DDYFDGYAMNLOQLKNMAEHIQAKA 442

Db 324 AEVCEEGVNAVHQTFFGALAAVSNLKKMSINPETKA 362

RESULT 13

S35157

Delta6 fatty acid desaturase (EC 1.14.99.-) [imported] - Synechocystis sp.

C:Species: Synechocystis sp.

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000

C:Accession: S35157; S76243

R:Reddy, A.S.; Nuccio, M.L.; Gross, L.M.; Thomas, T.L.

Plant Mol. Biol. 22, 293-300, 1993

A:Title: Isolation of a Delta(6)-desaturase gene from the cyanobacterium Synechocystis

A:Reference number: S35157; MUID:93283633

A:Accession: S35157

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-359 <RED>

A:Cross-references: GB:L11421; NID:g349562; PIDN:AAA27286.1; PID:g349563

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,

O, K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys

A:Reference number: S74322; MUID:97061201

A:Accession: S76243

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-359 <RED>

A:Cross-references: EMBL:D90914; GB:AB001339; NID:g1653477; PIDN:BAAL8502.1; PID:d101

A:Experimental source: PCC 6803

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 8.9%; Score 215.5; DB 2; Length 359;

Best Local Similarity 24.8%; Pred. No. 1.5e-09;

Matches 82; Conservative 62; Mismatches 145; Indels 41; Gaps 14;

Qy 126 FLFKAISTLSIMAFYQLYLGWYITSACLLALAWQFGLTHEFCHQOPTKRNPLNDTI 185

Db 50 WLSAWAFVLFPAPVIFPVRLLGCMWLALAAAFSN-----VGHANHNAYSSNPHIRVL 105

Qy 186 SLFFGNFLOGFSRDWKKDKHN-TTHAATNVIDHGDIDLAPLFAFIPGDLCKYKASFKA 244

Db 106 GMTY-DEV-GLSSFLWRYRHNLYLHHTYTNILGHDEIH-----GD-GAVRMSPEQE 153

Qy 245 ILKTVIPYQHLVFTAMLPMLRFSWTSQSVQWVFKENOMEYKYVQRNAF--NEQATVIG-HW 301

Db 154 HVGIVRQQFYWGLYLFIPFPWFLDYVYLV--NKGKYHDHKIPFPQPLELASLLGKL 211

Qy 302 AWVYQFLPLTPWPLRVAYFI-----ISQMGGLLIAHVVTFNH-----NSVDKYPA 348

Db 212 LMLGYVFGI-----PLALGFSIPEVLIGASVTYMTYGVCTIFMLAHVLESTEFITPDGE 267

Qy 349 NSRILNNAALQILTRNM-TPSPFIDWLWGLNGLYOIEHHLFPTMPCNLNACVKYKRW 407

Db 268 SGADDEWAICQIIRTANFATNPFNNFCGLNHQVTHLFPNICHIHYPQLENIKDV 327

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 01:31:09 ; Search time 2744.86 seconds
(without alignments)
11146.141 Million cell updates/sec

Title: us-09-555-093-1
Perfect score: 1462
Sequence: 1 gctccacaaatgtctgtcg.....aataaacctgttttcaa 1462

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_on.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
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- 19: em_mu.*
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- 21: em_ov.*
- 22: em_lo.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description

1	1451	99.2	1463	3	AF031477	AF031477	Caenorhabditis elegans delta6-fatty-acid-desaturase mRNA, complete cds.
2	1451	99.2	1463	6	AX003603	AX003603	Caenorhabditis elegans delta6-fatty-acid-desaturase mRNA, complete cds.
3	832.8	57.0	30748	3	CEW0802	CEW0802	Caenorhabditis elegans delta6-fatty-acid-desaturase mRNA, complete cds.
4	350.4	24.0	1461	3	AF114440	AF114440	Caenorhabditis elegans delta6-fatty-acid-desaturase mRNA, complete cds.
5	348.2	23.8	1344	3	AF078796	AF078796	Caenorhabditis elegans delta6-fatty-acid-desaturase mRNA, complete cds.
6	348.2	23.8	1344	6	AX020906	AX020906	Caenorhabditis elegans delta6-fatty-acid-desaturase mRNA, complete cds.
7	112.8	7.7	1275	8	AF139720	AF139720	Euglena grisea delta6-fatty-acid-desaturase mRNA, complete cds.
8	98.6	6.7	1374	8	AF465282	AF465282	Mortierella elongata delta6-fatty-acid-desaturase mRNA, complete cds.
9	97	6.6	1374	6	AR080598	AR080598	Sequence
10	97	6.6	1617	6	AR080598	AR080598	Sequence
11	97	6.6	1617	6	AR098439	AR098439	Sequence
12	97	6.6	1617	6	AR136018	AR136018	Sequence
13	97	6.6	1617	6	AF110510	AF110510	Mortierella elongata delta6-fatty-acid-desaturase mRNA, complete cds.
14	96.2	6.6	38060	3	CEP13F2	CEP13F2	Caenorhabditis elegans delta6-fatty-acid-desaturase mRNA, complete cds.
15	90.6	6.2	1374	8	AF307940	AF307940	Mortierella elongata delta6-fatty-acid-desaturase mRNA, complete cds.
16	90.6	6.2	1374	8	AF465281	AF465281	Mortierella elongata delta6-fatty-acid-desaturase mRNA, complete cds.
17	90.6	6.2	1947	8	AF465283	AF465283	Mortierella elongata delta6-fatty-acid-desaturase mRNA, complete cds.
18	89	6.1	1590	8	AB020032	AB020032	Mortierella elongata delta6-fatty-acid-desaturase mRNA, complete cds.
19	78.8	5.4	1546	8	AB052086	AB052086	Mucor circinellus delta6-fatty-acid-desaturase mRNA, complete cds.
20	76.2	5.2	2012	6	AX069275	AX069275	Sequence
21	76.2	5.2	2012	8	PPAJ2980	PPAJ2980	Physcomitrella patens delta6-fatty-acid-desaturase mRNA, complete cds.
22	75.4	5.2	1572	8	AF290983	AF290983	Mucor roumii delta6-fatty-acid-desaturase mRNA, complete cds.
23	75.4	5.2	1572	8	AF296076	AF296076	Mucor roumii delta6-fatty-acid-desaturase mRNA, complete cds.
24	68.8	4.7	1856	8	AF005096	AF005096	Ricinus communis delta6-fatty-acid-desaturase mRNA, complete cds.
25	68.4	4.7	1071	8	AF307941	AF307941	Mortierella elongata delta6-fatty-acid-desaturase mRNA, complete cds.
26	68.4	4.7	1644	8	AF307942	AF307942	Mortierella elongata delta6-fatty-acid-desaturase mRNA, complete cds.
27	68.4	4.7	1684	6	AR076814	AR076814	Sequence
28	68.4	4.7	1684	6	AR084177	AR084177	Sequence
29	68.4	4.7	1685	6	AR020904	AR020904	Sequence
30	68.4	4.7	1685	6	I38430	I38430	Sequence 4
31	68.4	4.7	1685	8	AF007561	AF007561	Borago officinalis delta6-fatty-acid-desaturase mRNA, complete cds.
32	68	4.7	1687	8	BOU79010	BOU79010	Sequence
33	62.6	4.3	1478	8	AY055117	AY055117	Echium plantaginum delta6-fatty-acid-desaturase mRNA, complete cds.
34	62	4.2	1467	6	AX058832	AX058832	Sequence
35	62	4.2	2040	6	AX058830	AX058830	Sequence
36	62	4.2	2040	8	CPU250734	CPU250734	Sequence
37	61.4	4.2	1450	8	AY055118	AY055118	Echium plantaginum delta6-fatty-acid-desaturase mRNA, complete cds.
38	56.2	3.8	1678	6	AX007241	AX007241	Sequence
39	56.2	3.8	1704	8	AF428420	AF428420	Arabidopsis thaliana delta6-fatty-acid-desaturase mRNA, complete cds.
40	56.2	3.8	1705	8	ATAJ4161	ATAJ4161	Arabidopsis thaliana delta6-fatty-acid-desaturase mRNA, complete cds.
41	56.2	3.8	95993	8	ATF2A19	ATF2A19	Arabidopsis thaliana delta6-fatty-acid-desaturase mRNA, complete cds.
42	55.8	3.8	2160	6	AX058840	AX058840	Sequence
43	55.8	3.8	2160	8	CPU250735	CPU250735	Sequence
44	51.8	3.5	1141	6	AX083744	AX083744	Sequence
45	51.8	3.5	1508	10	AF126798	AF126798	Mus musculus delta6-fatty-acid-desaturase mRNA, complete cds.

ALIGNMENTS

RESULT	1	AF031477	1463 bp	mRNA	linear	INV 02-MAY-1998
LOCUS	AF031477	Caenorhabditis elegans delta6-fatty-acid-desaturase mRNA, complete cds.				
DEFINITION	AF031477	GI:3088519				
ACCESSION	AF031477					
VERSION	AF031477.1					
KEYWORDS						
SOURCE		Caenorhabditis elegans.				
ORGANISM		Caenorhabditis elegans				
REFERENCE	1	(bases 1 to 1463)				
AUTHORS		Savanova, O., Smith, M.A., Lapinskas, P., Stobart, A.K., Dobson, G., Christie, W.W., Shewry, P.R. and Napier, J.A.				
TITLE		Expression of a borage desaturase cDNA containing an N-terminal cytochrome b5 domain results in the accumulation of high levels of delta6-desaturated fatty acids in transgenic tobacco				
JOURNAL		Proc. Natl. Acad. Sci. U.S.A. 94 (8), 4211-4216 (1997)				
MEDLINE		97268723				
REFERENCE	2	(bases 1 to 1463)				
AUTHORS		Napier, J.A., Hey, S.J., Lacey, D.J. and Shewry, P.R.				
TITLE		Identification of a caenorhabditis elegans				

April 97

Delta6-fatty-acid-desaturase by heterologous expression in
saccharomyces cerevisiae
Biochem. J. 330 (Pt 2), 611-614 (1998)
98149727
3 (bases 1 to 1463)
Napier, J.A.
Direct Submission
Submitted (27-OCT-1997) Cell Biology, IACR-Long Ashton Research
Station, Long Ashton, Bristol BS18 9AF, UK
Location/Qualifiers
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/chromosome="IV"
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QQQGLWLFECFOQPKNRPNZLISLFFNGFLQFSRWWKKHWHHAATHVNDHID
DLDLAPLFAFIPDGJCKYKASFEKAILKIVPOHLYFTAMLPMLEFRSMTGQSVQWVF
KENOMEKVYORNAFEQATIVGHAWVFQLELLFTWPLRVAYFTISOMGGGLLIAH
VVFTHNSVDKYPSNKRILNNFAALQILTRNNMTPSPFIDLWGGGLNYQIEHHLFPTM
PRCLNLSNVKVVYKKNLPLVLDVDFDYGAMNQLKKNMAEHIQAKAA"

BASE COUNT 445 a 288 c 277 g 453 t

ORIGIN

Query Match 99.2%; Score 1451; DB 3; Length 1463;
Best Local Similarity 99.9%; Pred. No. 2.6e-310;
Matches 1462; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Db	61	ATGGCTCTACCTTAGCAGGAATTGGTGAAGAAACATCCAGGAGGAGCTGTATTGAACA	120
Qy	121	atagaaaattcgatgctactcatatttccacgctttccacgaagatcttctcaggc	180
Db	121	ATATAGAAATTCGATGCTACTCATATTTTCCACGCTTTCCACGAAGATCTTCTCAGGC	180
Qy	181	ttataagcaacttgaccttctgaaaaacgacggagacagatgaattccttgagaaca	240
Db	181	TTATAGCAACTTGACCTTCTGAAAAACGAGGAGACGATGAATTCCTTGAGAAACA	240
Qy	241	attgaaaaagacacttgacaaagtgtatcaattgtatcagcatatgatgtcagtggtgc	300
Db	241	ATTGAAAAAGAGACTTGACAAAGTTGTATATCAATGTATCAGCATATGATGTCAGTGTGC	300
Qy	301	acaagaaagaaatggttgaatcattccgaaactacgacagaagcttcgatgatgg	360
Db	301	ACAAGAAAGAAAATGGTTGAATCATTCGAAAAACTACGACAGAAGCTTCATGATGATGG	360
Qy	361	attaatgaagcaaatgaacaatatcttcctgttttaagcagattccaactttcaattat	420
Db	361	ATTAAATGAAGCAAAATGAACATATATTCCTGTTTAAAGCGAATTTCAACACTTTCAAATTAT	420
Qy	421	ggcatttgcatcttcttcagtatcttggatgggtattactactctgcattgtttattagc	480
Db	421	GGCATTTGCATTTTATCTTCAGTATCTTGGATGGTATATTACTTCTGCATGTTTATTAGC	480
Qy	481	acttgatggcaacaattcggatgggttaacacatgadtcttgcatacaacgacaca	540
Db	481	ACTTGATGGCAACAATTTCGGATGGTGTAAACACATGAGTCTTGCCATCAACAGCAACAAA	540

ORGANISM

Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 1463)

REFERENCE

Napier,J.A.

AUTHORS

Desaturase genes and their use

TITLE

Patent: WO 99/27111-A 1 03-JUN-1999;

JOURNAL

UNIV BRISTOL (GB); NAPIER JOHNATHAN A (GB)

FEATURES

Location/Qualifiers

source

1..1463

/organism="Caenorhabditis elegans"

/db_xref="taxon:6239"

CDS

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BASE COUNT 445 a 288 c 277 g 453 t

ORIGIN

Query Match

Best Local Similarity 99.2%; Score 1451; DB 6; Length 1463;

Matches 1462; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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RESULT 3

CEW08D2

LOCUS

Caenorhabditis elegans cosmid W08D2, complete sequence.

DEFINITION

270271.1 GI:1236102

ACCESSION

HTG; Collagen; Human myeloid cell line protein like; Transporter

KEYWORDS

ATPase like; Tyrosine-protein kinase; WNT protein.

SOURCE

Caenorhabditis elegans.

ORGANISM

Caenorhabditis elegans.

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;

Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

REFERENCE AUTHORS TITLE	1 (sites) none.	4202. .4479,4668. .5004,6413. .6748,6795. .6896,7376. .7420))
JOURNAL MEDLINE	Genome sequence of the nematode <i>C. elegans</i> : a platform for investigating biology. The <i>C. elegans</i> Sequencing Consortium Science 282 (5396), 2012-2018 (1998)	/gene="w08d2.3"
REMARK	99069613	/note="predicted using Genefinder"
REFERENCE AUTHORS TITLE	The <i>C. elegans</i> Sequencing Consortium. 2 (bases 1 to 30748) Swinburne,J. and Ainscough,R. Direct Submission Submitted (23-MAR-1996) Nematode Sequencing Project, Sanger Institute, Hinxton, Cambridge CB10 1SA, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rwnematode.wustl.edu Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other available information. Current sequence finishing criteria for the <i>C. elegans</i> genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note. IMPORTANT: This sequence is not the entire insert of clone w08d2. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions. The true left end of clone w08d2 is at 1 in this sequence. The true right end of clone w08d2 is at 5560 in sequence w07284. The true left end of clone w07f5 is at 30645 in this sequence. The start of this sequence (1. .108) overlaps with the end of sequence z81122. The end of this sequence (30645. .30748) overlaps with the start of sequence w07284. 960307: Dual authors: June Swinburne & Rachael Ainscough For a graphical representation of this sequence and its analysis see: http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?name=w08d2 IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions. Location/Qualifiers 1. .30748 /organism="Caenorhabditis elegans" /db_xref="taxon:6239" /chromosome="IV" /clone="w08d2" join(21. .59,907. .983,1289. .1784,2096. .2224,2272. .2572,2623. .2729,2775. .2957) /gene="w08d2.4" join(21. .59,907. .983,1289. .1784,2096. .2224,2272. .2572,2623. .2729,2775. .2957) /gene="w08d2.4"	/protein_id="CAA94232.1" /db_xref="GI:3880556" /db_xref="SPTREMBL:Q23220" /translation="MPIEVNDFYDPAYHPKPIFORIVEAKETASKHPSLFIHLWIYS LIGTWTFTISLSYSHSACYMISSAHLNLFHFAFNGLSGLSAVINSVVFVKQSFLL ITCLILISACFLAPHAHAHITLLCIVIFVFGTGLISLAVINSVVFVKQSFLL QFLHLGAFGSVTAVMPYQSAPESEHQEDCKSRNPVLPCTGPHIPSLKPYLNPSLROD QQDSVSLKVLVCSVASIANIMTFFPFLIQAQSPASIFYIYOLFVSKQKQFYK GFYQIFFFMGVIRAYSLFSYDMPYFVFGSIFGCGGCCCAISEQLVGLSLFGFF LAPLLPVIYIHNHLSLKNSMTFTLLSGHSGHLIPFLTLTNSNSRSLRIFAQNFV AIVTLVILSILSHAQIERMOASQGLNLFVSRFLSGESLLKRTSRIPLSRLRP NSYRFRANRGLNTRSPSPAVPHSTEVSDLSRLNEKPEKIRSGSMLMTRY"
COMMENT	gene CDS	complement(join(10141. .10236,10563. .10663,10723. .10849,10969. .11112,11159. .11329,11379. .11518,11918. .12000,12059. .12138,12192. .12324,12373. .12479)) /gene="w08d2.1" complement(join(10141. .10236,10563. .10663,10723. .10849,10969. .11112,11159. .11329,11379. .11518,11918. .12000,12059. .12138,12192. .12324,12373. .12479)) /gene="w08d2.1" /note="Similarity to Mouse WNTB protein (SW:WNTB_MOUSE), contains similarity to Pfam domain: PF00110 (wnt family of developmental signaling proteins), Score=366.8, E-value=1.6e-133, N=1" /codon_start=1 /protein_id="CAB61041.1" /db_xref="GI:6434322" /db_xref="SPTREMBL:Q9TVJ1" /translation="MORFICILFVLLVGYQSPSATYSTQVYNWMLTLAFVGSN DYLPKPHSTDRHFKELCRRLDGLNPQAALCAENPFSPFVARGVREIRECENK FKPERKCSSRDEVTRTHGFRQDILKRLSKANKRAFLNMAASLIVHSITGCTF GNLTECCGDSKPGMORYQASDPSMRDQFSWGGSDNPHGIRYAKFLDDWETAQF DKTYNVAHLVRRHNNFVGREAIQAQIRQCRCGHVSGCEFTCLQMKFSQVSDLL KKRYDFAVQVTRKATRKLRKTERKIPLRGNEMAYVHRSPSYCEKNLTAGILGTS GRECIHNSYSSCDLLCCGRGYNTRLEIROTCCKFVWCCEVKCTCTEEVAHTC K"
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AUTHORS	Watts,J.L. and Browse,J.			
TITLE	Isolation and characterization of a Delta 5-fatty acid desaturase from Caenorhabditis elegans			
JOURNAL	Arch. Biochem. Biophys. 362 (1), 175-182 (1999)			
MEDLINE	91117288			
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AUTHORS	Watts,J.L. and Browse,J.			
TITLE	Direct Submission			
JOURNAL	Submitted (16-DEC-1998) Institute of Biological Chemistry, Washington State University, Clark Hall, Pullman, WA 99164-6340, USA			
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BASE COUNT	426 a	292 c	273 g	470 t
ORIGIN				

Query Match		24.0%;	Score 350.4;	DB 3;	Length 1461;
Best Local Similarity		54.6%;	Pred. NO. 3.1e-67;		
Matches 749;		Conservative	0;	Mismatches 611;	Indels 12; Gaps 2;
Qy	44	atgaaggtcgatggaacaaatgctctaccccttagcgaggaatggtgaaagaacacatccagga	103		
Db	79	ATTAATAATTGGAATAATGGTGTCAAATTCACGATGTGTCTCTGAGATCATCCAGT	138		
Qy	104	ggagctgttattgaaacaatatagaattcgatgctactcatattttccacgctttccac	163		
Db	139	GGTAGTGCATTTACTACCTATATAAAATATGGATGCGCACTACCGTATTCACACATTCAT	198		
Qy	164	gaagatctctcagcgttataagcaacttgaccttctgaaaaagcagcg- - - - -agag	217		
Db	199	ACTGTTCTTAAGAAGCGCTATCAATGGCTGACAGAAATTTGAAAAAGAGTGCCCTACACAA	258		
Qy	218	cacgatgaattccttgagaacaattggaaaagagacttgacaaagtgtgatcaatgta	277		
Db	259	GAACCAGAGATCCCAGATATTAAAGGATGACCCAATCAAGGAATTTGATGATGTGAACATG	318		
Qy	278	tcagcatatgatgtcagtggttgacagaaaagaaatggttgaaatcattcgaaaaacta	337		
Db	319	GGACTTTCAATATTTCTGAGAAACGATCTGCCCAATAATAATAAAGTTTCTACTGATCTA	378		
Qy	338	cgacagaagcttcgatgatgattgaatgaaagcaaatgaaacatatattccctgtttaaa	397		
Db	379	CGTAGTCGAGTTTCGTCGACGAAGGACTTATGGATGGATCTCCTTTTCTTACATTAGAAA	438		
Qy	398	gcgatctcaaacacttcaattatggcattttatcttctcagtatcttggatggtat	457		
Db	439	ATTCTTGAACAATCTTCACAAATCTTTTTCATTTCTACCTTCAATACACACATATTAT	498		
Qy	458	attactctcatgtttattagcacttcgacgcaaatcggatcggttaacacatgaag	517		
Db	499	CTTCATCAGCTATTCTAATGGGATTCGTCGGCAACAATTTGGGATGTTTATCCATGAA	558		
Qy	518	ttctgccatacacgcccaacaagaacagacctttgaaatgatactattttcttcttctt	577		
Db	559	TTGCGCATCATCAGTTCTTCAAAAACAGATACATACAAATGATTGTGGCCAGCTATTTCGT	618		
Qy	578	ggttaattcttacaaggatttttcaagagatggtggaaggcaacatacaacatcacac	637		
Db	619	GGAAACTTTTACAGAGATTCTCATCTGCTGGTGTGGAAGAGACGACACATGTGTCATC	678		
Qy	638	gctgccacaatgtaattgatcagcgtaatcgcacttggcaccacttttcgcat	697		
Db	679	GCAGCCACAATGTGTTGGAGAGCGGAGATCTTGATTATTAGTCCCATTTCTATGCTACA	738		
Qy	698	attccaggagatttgtcaagtataaggccagctttgaaaaagcaattctcaagattgta	757		
Db	739	GTGGCAGAACATCTCAACAATATTCT- - - - -CAGGATTTCATGGGTTATGACTCTATTTC	792		
Qy	758	ccatatcaacatctctatttccacgcgaatgcttccaatgctcgttctctcatggaactggt	817		
Db	793	AGATGGCAACATGTTTCATTGGACATTCATGTTACCATTTCTCCCGTCTCGTGGCTCTT	852		
Qy	818	cagtcagttcaatgggtatttcaagagaaatcaaatggagatcaaggtctatcaagaataat	877		
Db	853	CAGTCATCATTTTGTGTAGTCAGATGCCAACTCATTTATTATGACTATTACAGAAATACT	912		
Qy	878	gcattctgtgggagcaagcaacaatttgttgacattgggcttgggtattctataattgttc	937		
Db	913	CGCATTTATGAACAGTTGGTCTCTCTTTGCATGGGCTTGTGCTATTGGGTCAATTTGAT	972		
Qy	938	ttattaccaacatggcgaactcgggtgcttatttcatatttcaacaataatgggaagagcc	997		
Db	973	TTCTCCCGGATGTGCAACTAGATAATATGTTCTCTCTTCTTCATCTTTGTTGGAGGT	1032		
Qy	998	cttttgatgctcacgtagtcactttcaaccataactctgttgataagtatccagccaat	1057		
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Db 1051 TCGAATCATGTCFAAATTTACGCTTGTCTCAAAATCATGACCACAAAGAAATATGAGACCT 1110
QY 1118 tctccattcattgattggcttggggtggactcaattatcagatcgagcaccacttgctc 1177
Db 1111 GGAAGATTCAATGACTGGCTTTGGGAGGTCTTAATCAATCAGATGAGCACCATCTTTTC 1170
QY 1178 ccaacaatgccagcttgcaatctgaatgcttgcgtgaaatatgtgaaagaattggtgcaa 1237
Db 1171 CCAACGATCCAGCAGACAACTTGAACACTGTATGCCACTTGTAAAGGAGTTTGAGCA 1230
QY 1238 gagaataatcttcccttaactcgatgactactcttgaacggatatacgaaatgaatttgcaa 1297
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RESULT 6
AX020906
LOCUS AX020906 1344 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 2 from Patent WO9933958.
ACCESSION AX020906
VERSION AX020906.1 GI:10044591
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1344)
AUTHORS Michaelson,L., Stobart,K. and Napier,J.A.
TITLE Desaturase
JOURNAL Patent: WO 9933958-A 2 08-JUL-1999;
MICHAELSON LOUISE (GB); STOBART KEITH (GB); UNIV BRISTOL (GB);
NAPIER JOHNATHAN A (GB)
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source Location/Qualifiers
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ORIGIN

Query Match 23.8%; Score 348.2; DB 6; Length 1344;
Best Local Similarity 55.8%; Pred. No. 9.7e-67;
Matches 712; Conservative 0; Mismatches 553; Indels 12; Gaps 2;

QY 44 atgaaggtcgatggcaaatgctctaccttagcagggaattggtgaagaacatccagga 103
Db 37 ATTAATAATTGATGGAAAATGGGTCAAAATGACATGATGCTGCTCGATGACATCCAGGT 96
QY 104 ggagctgttatgaacaaatagaaattggatgctactcatatatttccacgctttccac 163
Db 97 GGTAGTCAATTAATCTACTACCTATAAAATATGGATGGCACTACCGTATTTCCACATTCAT 156
QY 164 gaaggtcttctcaggtcttaagaacacttgacctctctgaaagaagcaagg-----agag 217
Db 157 ACTGGTCTTAAAGAGACGGTATCAATGGCTGACAGAATTGAAAAAAGAGTGCCTACACAA 216
QY 218 cagcatgaattccttgagaaacaattggaaaagagacttgacaaagtgtgatcaatgta 277
Db 217 GAACAGAGATCCAGATATTAGAGTAGACCAATCAAGGAATTGATGATGTGACATG 276
QY 278 tcagcatgatgtcagttgtgcacaaagaaagaaatggttgaatcattcgcgaaaaacta 337
Db 277 GGAATTTCAATATTCTTCAGAAACGATCTGCCCAATAAATAAAGTTTCACTGATCTA 336
QY 338 cgacagaagcttcatgatgatgatttaataatgaagaacaaatgaacatatatttctgttaa 397

Db 337 CGTATCGGAGTTTCGTGCAGAAGGACTTATGGATGGATCTCCCTTTGTTCTACATTAGAAAA 396
QY 398 gggatttcaaacactttcaattatgacatttgcattttatcttcaagtatcttgcagtggtat 457
Db 397 ATTCFTGAAACAATCTTCACAATTCCTTTTGGATTCTACCTTCAATACCACACATATTAT 456
QY 458 attactctgcagtgtttattagcacttgatggcaacaattcggatggttgaacacatgag 517
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QY 518 ttctgcattcaacagacccaacaagaacacotcttgaatgatatactattcttctgttcttt 577
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QY 578 ggttaatttctcaagagattttcaagagatttgggtgaagacaagaacataaacactcatc 637
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Db 751 AGATGGCAACATGTTCAITTTGGACATTCATGTTACCATTCCTCCGCTCTCTCGTGGCTCTT 810
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QY 1178 ccaacaatgccagcttgaatctgaatgcttgcgtgaaatatgtgaaagaattggtgcaa 1237
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QY 1238 gagaataatcttcccttaactcgatgactactcttgaacggatatacgaaatgaatttgcaa 1297
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QY 1298 caattgaaaaatatggc 1314
Db 1291 CAATTCGGAATATTGC 1307

RESULT 7

AF139720
LOCUS AF139720 1275 bp mRNA linear PLN 29-JUL-1999
DEFINITION Euglena gracilis delta8 fatty acid desaturase (efdl) mRNA, complete cds.
ACCESSION AF139720

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VERSION      AF139720.1  GI:5639723
KEYWORDS
SOURCE       Euglena gracilis.
ORGANISM     Euglena gracilis
             Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.
REFERENCE    1 (bases 1 to 1275)
AUTHORS      Wallis,J.G. and Browse,J.
TITLE        The Delta8-desaturase of Euglena gracilis: an alternate pathway for
             synthesis of 20-carbon polyunsaturated fatty acids
JOURNAL      Arch. Biochem. Biophys. 365 (2), 307-316 (1999)
MEDLINE      99262077
PUBMED       10328826
REFERENCE    2 (bases 1 to 1275)
AUTHORS      Wallis,J.G. and Browse,J.
TITLE        Direct Submission
JOURNAL      Submitted (29-MAR-1999) Institute of Biological Chemistry,
             Washington State University, 441 Clark, Pullman, WA 99164-6340, USA
FEATURES
source       1..1275
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gene         1..1275
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             ETMNRIGITIDWFEGGLNYQIEHLNPTPLPHNLTAVSIVQEQLCKQHNLPIRNLPLP
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BASE COUNT  294 a 326 c 327 g 328 t
ORIGIN

Query Match      7.7%; Score 112.8; DB 8; Length 1275;
Best Local Similarity 48.3%; Pred. No. 9.5e-15;
Matches 389; Conservative 0; Mismatches 402; Indels 15; Gaps 2;

QY 454 qtatattactctgcagtttattagcacttcgacggaacattcggttggttaacaca 513
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 382 GTATTTCATTGGGCGCAGTGTGCTGGGATGCACATATCAACAGATGGCTGTTCTCA 441
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QY 514 tgagttctgccatcaacagccaacagaacagacctttgaatgatactattcttgtt 573
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DB 442 TGACATTTGCCACCACCACACATTTCAAGAACCGGAACCTGGAAACCTCGTGGGACTGGT 501
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QY 574 ctttggaatttttacaaggatttttcaagagattggttgaaggacaagcataactca 633
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DB 502 ATTTGGCAATGTCTGCAAGTGTTCCTCGTGACATTTTGAAGGACAGACACAATGCACA 561
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QY 634 tcacgctgcacaaatgtaattgatcatcagcgttgatcatcacttggcaccatttcc 693
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DB 562 TCATTGGCAACCAATGTTCAAGGCGGACGCCCTGATATGACAACTCCCCCTTAGC 621
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QY 694 atttattccaggagattgtgcaagtataaggccagctttgaaaagcaattctcaagt 753
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DB 622 CTGGTCTGAGGATGACGTCACACGGGCGTCACCGATTT-----CCGCGAAGCT 669
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QY 754 tgtaccataatacactctctatttaccgccaatgcttccaatgctccgtttctcatggac 813
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DB 670 CATTCAGTTCACAGCAGTACTATTCTTGCTCATCTCTATCTTGTTCGCGTTATTGGTG 729
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QY 814 tggtcagtcagttcaatgggtattcaagaagaatacaaatcaaatggagtacaaggtctatcaag 873
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DB 730 TTTCCAGTCGCGTTGACCGTCGCCAGTGTGAAGGACAGAGATAACCAATTCATCGCTC 789
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QY 874 aaatgcattctctggagacaagcaaaattgttgacatttgggcttg---ggtattctatca 930
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DB 790 TCAGTATAAGAGAGGAGGCCATTGGCCCTCGCCCTGCACTGGACACCTTGAGGCCCTGTTC 849
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DB 850 CTATTATCTTTATATCCAGCATCTCATACGCTGTTGGTGTGTTTTCGTTTCGGAGCTGGT 909
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DB 970 GGACCCAGCTCTGGATGGCCATGGATTCTCGGTTGGCCAGATCCATGAGACCATGAACAT 1029
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QY 1111 gactccatctccattcattgattggttgggtggactcaaatatcagatcagacaacca 1170
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QY 1171 cttgttcccaacaatgccacgttgcaatcgtcgtgctgctgctgctgctgctgctgctg 1230
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DB 1090 TTTGTGCGCGACCCCTCCCTGCCACACACCTGACAGCGGTTAGCTACCGAGTGGACACGCT 1149
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QY 1231 gtgcaaaagagaataaattcttcttacc 1256
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DB 1150 GTCCAGAGACACACACCTGCCGTTATC 1175
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RESULT      8
AF465282
LOCUS       Mortierella isabellina delta 6 fatty acid desaturase (GLD6D) gene,
DEFINITION complete cds.
ACCESSION  AF465282
VERSION     AF465282.1  GI:18483176
SOURCE      Mortierella isabellina.
ORGANISM    Mortierella isabellina
            Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales;
            Mortierellaceae; Mortierella.
REFERENCE   1 (bases 1 to 1374)
AUTHORS     Xing,L., Liu,L., Li,M. and Hu,G.
TITLE       Cloning and sequence analysis of the delta 6 fatty acid desaturase
            gene from Mortierella isabellina M6-22 genomic and cDNA
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 1374)
AUTHORS     Liu,L., Li,M., Hu,G. and Xing,L.
TITLE       Direct Submission
JOURNAL     Submitted (04-JAN-2002) Microbiology, Naikai University, Weijing
            road 94th, Tianjin 300071, China
FEATURES    Location/Qualifiers
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            gene
            CDS
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BASE COUNT 257 a 395 c 362 g 360 t
ORIGIN

Query Match 6.7%; Score 98.6; DB 8; Length 1374;
Best Local Similarity 47.3%; Pred. No. 1.3e-11;
Matches 416; Conservative 0; Mismatches 439; Indels 24; Gaps 3;

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DB 466 TCGGCTCGCCTCTTGCGTCTCTTCGGCAGCAGTGATGGTGGCGCACGACITTTTG 525

QY 524 catcaacagccaaacaaagacacctttgaatgatactattcttcttcttgtaatt 583
DB 526 CACCACACAGGTCTTCAGGACCGTTTCTGGGGTGATCTTTTCGGCGCCTCTTGGGAGGT 585

QY 584 ttcttacaaggattttcaagagatttggtgaaggaacagcataaacactcatcacgtgcc 643
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DB 706 CATGCTTTGGAGATGTTCTCGGACGTCCTCGACGAGGAGCTGACCGGACGTGTGGTCGCGC 765

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DB 766 TTCTATGTCCTTAACAGACACTGGTGTCTACTTCTCCCATTTCTCTGTTGCCGCTCTCTCC 825

QY 809 tggactggttcagtcagttccaatgggtatt-----caaagagaatacaaatggagtaacaag 862
DB 826 TGGTGCTCCAGTCCATCCTCTTTGTTCTGCTTAACGGTCAAGCGGCCACACAGCCCTCTGA 885

QY 863 gctatcaaaagaaatgcatcttgggagaagaacaaatggttggacacttgggcttgggta 922
DB 886 GCCCGTGTGCCCATTTCTCTTGGTCAGCAGAGCTGTCTTTCGCGCTGCACCTGGACCTGGTAC 945

QY 923 ttctatcaattgtcttattaccacatggccact---tcgggttgcttatttcaattatt 979
DB 946 CTCGCCACCATGTTCTGTTCATTAAAGACCCCGTCAACATGATGGTGACTTTTGGTG 1005

QY 980 tcacaaatggggaggcccttttattgctcagtagtcaactttcaaccataactctgtt 1039
DB 1006 TCTCAGGCTGTTTGGGGTAACCTGTGGCGATTGTCTTCGCTCAACCCACACGCTATG 1065

QY 1040 gataagtatccagcaaatctctgaatttttaaacacttgcgcgtcttccaaattttgacc 1099
DB 1066 CCTGTGATCTCAAGAGGAAAGCCGTCGACATGGATTCTTCACCAAGCAGATCATCAG 1125

QY 1100 acacgaacatgactccatctccattcatattgacttggcttgggtggactcaattatcaag 1159
DB 1126 GGTGCTGATGTTACCCCTGGTCTGTTCGCCAACTGGTTCACGGGTGATTGAACCTACAC 1185

QY 1160 atcgagcaccaacttgttcccaacaatgcccacgcttgcaatctgaaatgcttgcgtgaaatat 1219
DB 1186 ATTGAGCACCACTGTTCTCCCTTCGATGCCCTCGCCACAACTTTTCAAAGATCCAGCCTGCT 1245

QY 1220 gtgaagaatggtgcaagagaataatcttcttaccttgctcgatgactcaactttgacgga 1279
DB 1246 GTCGAGACCTTGTGCAAAAAGTATGGTGTCCGATACCCACACACTGGCATGATCGAGGGA 1305

QY 1280 tatgcaatgaaattgcaacaattgaaaaatatggctgag 1318
DB 1306 ACTGCAGAGGTCTTTAGCGGTTTGACAGGCTCTCCAAG 1344

RESULT 9
AF306634
LOCUS
DEFINITION
Mortierella isabellina delta6-fatty acid desaturase mRNA, complete cds.
ACCESSION AF306634
VERSION AF306634.1 GI:11559823
KEYWORDS
SOURCE Mortierella isabellina.
ORGANISM Mortierella isabellina
Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales;
Mortierellaceae; Mortierella.
REFERENCE 1 (bases 1 to 1374)
AUTHORS Ming-Chun, L., Li, L., Guo-Wu, H., Li, Z. and Lai-Jun, X.
TITLE Cloning and sequencing analysis of delta6-fatty acid desaturase gene from Mortierella isabellina
JOURNAL Junwu Xitong (2001) In press
REFERENCE 2 (bases 1 to 1374)
AUTHORS Ming-Chun, L., Li, L., Guo-Wu, H., Li, Z. and Lai-Jun, X.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2000) Department of Microbiology, Nankai University, 94 Weijin Road, Tianjin 300071, People's Republic of China
FEATURES
source Location/Qualifiers
1..1374
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/db_xref="taxon:91625"
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/product="delta6-fatty acid desaturase"
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EFVDPHPGGSVILTHVGKDGTDVDFTHPEAAWETLANFYVGDIDESTRAIKNDDFAA
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CLQSILLVLPNGQAHKPSGARVISLSVQLSLAHVHTWYLATMFLFIKDPVNMVMYFL
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BASE COUNT 260 a 393 c 359 g 362 t
ORIGIN
Query Match 6.6%; Score 97; DB 8; Length 1374;
Best Local Similarity 47.2%; Pred. No. 2.9e-11;
Matches 415; Conservative 0; Mismatches 440; Indels 24; Gaps 3;

QY 464 tctgcattgtttattagcacttcgacgaacattcgatggtggttaacacatgattctgc 523
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DB 706 CATGCTTTGGAGATGTTCTCGGACGTCCTCGACGAGGAGCTGACCGGACGTGTGGTCGCGC 765

QY 749 aagattgtaccataatacattcttattccacgaactgtcttccaaatgctcgttttcca 808
DB 766 TTCTATGTCCTTAACAGACACTGGTGTCTACTTCTCCCATTTCTCTGTTGCCGCTCTCTCC 825

QY 809 tggactggttcagtcagttccaatgggtatt-----caaagagaatacaaatggagtaacaag 862
DB 826 TGGTGCTCCAGTCCATCCTCTTTGTTCTGCTTAACGGTCAAGCGGCCACACAGCCCTCTGA 885

QY 863 gctatcaaaagaaatgcatcttgggagaagaacaaatggttggacacttgggcttgggta 922
DB 886 GCCCGTGTGCCCATTTCTCTTGGTCAGCAGAGCTGTCTTTCGCGCTGCACCTGGACCTGGTAC 945

QY 923 ttctatcaattgtcttattaccacatggccact---tcgggttgcttatttcaattatt 979
DB 946 CTCGCCACCATGTTCTGTTCATTAAAGACCCCGTCAACATGATGGTGACTTTTGGTG 1005

QY 980 tcacaaatggggaggcccttttattgctcagtagtcaactttcaaccataactctgtt 1039
DB 1006 TCTCAGGCTGTTTGGGGTAACCTGTGGCGATTGTCTTCGCTCAACCCACACGCTATG 1065

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DB 1066 CCTGTGATCTCAAGAGGAAAGCCGTCGACATGGATTCTTCACCAAGCAGATCATCAG 1125

QY 1100 acacgaacatgactccatctccattcatattgacttggcttgggtggactcaattatcaag 1159
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DB 1186 ATTGAGCACCACTGTTCTCCCTTCGATGCCCTCGCCACAACTTTTCAAAGATCCAGCCTGCT 1245

QY 1220 gtgaagaatggtgcaagagaataatcttcttaccttgctcgatgactcaactttgacgga 1279
DB 1246 GTCGAGACCTTGTGCAAAAAGTATGGTGTCCGATACCCACACACTGGCATGATCGAGGGA 1305

QY 1280 tatgcaatgaaattgcaacaattgaaaaatatggctgag 1318
DB 1306 ACTGCAGAGGTCTTTAGCGGTTTGACAGGCTCTCCAAG 1344

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Qy	863	gtctatcaagaataatgcattctgggagcaagaacaattgttggacattggggttggtta	922
Db	886	GCCCGGTGTCTCCATTTCTTGGTTCGAGCAGCTGTCTTGCATGCACCTGGGTATC	945
Qy	923	tcttatcaattgttcttattaccaaatggccact---tcgggtgtcttatttcattatt	979
Db	946	CTCGCCACCATGTTCTGTGTTCATTAAGGACCCCGTCAACATGATGTGTACTTTTGGTG	1005
Qy	980	tcacaaatgggagggcccttttggatgtcacgtagtcacatttcaaccataactctgtt	1039
Db	1006	TCTCAGGCTGTTTGGCGTAACCTGTTGGCGATTGTGTCTCGCTCAACACACAGCTATG	1065
Qy	1040	gataagtatccagccaattctcgaatttttaacaaacttcgcgcgtcttcaaaattttgacc	1099
Db	1066	CCTGTGATCTCCAAGGAGGAAGCCGTCGACATGGATTCTTCAACCAAGCAGATCATCAG	1125
Qy	1100	acacgcaacatgactccatctccattcattgtatgtgtcagtgtagtcaacttcaaccataactctgtt	1159
Db	1126	GGTGTGATGTTACACCTCGTCTGTTCGCCAATGTGTTACCGGTGGATTTGAACCTACCAG	1185
Qy	1160	atcgagcaccaactgttcccaacaatggccacgttgcaatctggaatcttcgctgagaaatat	1219
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Qy	1220	gtgaaagaatgtgcaagagagaataattcttcaactcgtctcgatgactcaactttgacgga	1279
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DEFINITION	Sequence 1 from patent US 5968809.		
ACCESSION	AR080598		
VERSION	AR080598.1	GI:10007328	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 1617)		
AUTHORS	Knutzon,D., Mukerji,P., Huang,Y., Thurmond,J. and Chaudhary,S.		
TITLE	Methods and compositions for synthesis of long chain poly-unsaturated fatty acids		
JOURNAL	Patent: US 5968809-A 1 19-OCT-1999;		
FEATURES	Location/Qualifiers		
source	1..1617		
BASE COUNT	310 a 470 c 410 g 427 t		
ORIGIN	/organism="unknown"		
Query Match 6.6%; Score 97; DB 6; Length 1617;			
Best Local Similarity 47.2%; Pred. NO. 2.9e-11;			
Matches 415; Conservative 0; Mismatches 440; Indels 24; Gaps 3;			
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Db	536	TCGGGTGCGCTTTTGGGTCTGTTCGGCAGCAGTCCGGATGTGCTCAGCACTTTTGG	595
Qy	524	catcaacagccaacaagaacagacctttgaatgatactattcttcttcttggtaaat	583
Db	596	CATCACCAGGTCTTCCAGGACCGTTCTGGGGTGATCTTTTCGGCGCCCTCTTTGGGAGGT	655

Qy	584	ttcttaaggattttcaagagagattggtggaagcaagcatacaactcatcactgcgtgcc	643
Db	656	GTCTGCCAGGGCTTCTCGTCTCGTGAAGGACAAGCACAACACTCACCACCGCGCC	715
Qy	644	acaaatgtaattgatcatgacgggtgatatgcacttggcaccactttttcgattattcca	703
Db	716	CCCAAGCTCCACGGCGAGGATCCCGACATTGACACCCACCCTCTGTGTGACCTGGAGTGAG	775
Qy	704	ggagatttggcaagtataaaggccagctttgaaaaagcaat-----tctc	748
Db	776	CATGCCGTTGGAGATGTTCTCGGATGTCCTCCAGATGAGGAGCTGACCCGCATGTGGTCCGCT	835
Qy	749	aagattgtaccatatcaacatctctatttcaocgcgaatgcttcccaatgcctccatgtcttctca	808
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Qy	809	tggactgggtcagtcagttcaattgggtatt-----caaagagaatcaaatggagtagacaag	862
Db	896	TGGTGCTCCAGTCCATTTCTTGTGCTGCTTAACGGTCAAGCCCAACAGCCCTCGGGC	955
Qy	863	gtctatcaagaataatgcattctggtgagcaagaacaattgttggacattggggttggtta	922
Db	956	GCGCGTGTCCCATCTCGTTGGTTCGAGCAGCTGCTCGTTCGGATGCACCTGGACTGGTAC	1015
Qy	923	tctatcaattgttcttattaccaacatggccact---tcgggtgtcttatttcattatt	979
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Qy	980	tcacaaatgggagggcccttttggatgtcagtagtcaacttcaaccataactctgtt	1039
Db	1076	TGCGAGCGGTGTGCGGAAACTTGTGTTGGCGATCGTGTCTCGCTCAACACACAGGTATG	1135
Qy	1040	gataatgtatccagccaattctcgaatttttaacaaacttcgcgcgtcttcaaaattttgacc	1099
Db	1136	CCTGTGATCTCGNAGGAGGCGGTGCGATATGGATTTCTTACGAGGAGATCATCAG	1195
Qy	1100	acacgcaacatgactccatctccattcattgtatgtgttgggttgggtggaactcaattatcag	1159
Db	1196	GGTGTGATGTCCACCGGGTCTATTGTCACACTGGTTCACGGGTGATTGAACACTATCAG	1255
Qy	1160	atcgagcaccaactgttcccaacaatggccacgttgcaatctggaatctggaatctgctgaaatat	1219
Db	1256	ATCGAGCACCACTGTTTCCCTTCGATGCTCGCCACAACCTTTTCAAGATCCAGCCCTGCT	1315
Qy	1220	gtgaaagaatgtgcaagagagaataattcttcaactcgtctcgatgactcaactttgacgga	1279
Db	1316	GTGAGACCCCTGTGCAAAAAGTACATGTCCGATACCAACACACCGGTATGATCGAGGGA	1375
Qy	1280	tatgcaatgaatttgcaacaattgaaaaatatggctgag	1318
Db	1376	ACTGCAGAGGTCTTTAGCCGTTTGAACGAGGCTCTCCAAG	1414
RESULT 11			
LOCUS	AR098439	1617 bp	DNA linear PAT 14-FEB-2001
DEFINITION	Sequence 1 from patent US 6075183.		
ACCESSION	AR098439		
VERSION	AR098439.1	GI:12807696	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 1617)		
AUTHORS	Knutzon,D., Mukerji,P., Huang,Y., Thurmond,J. and Chaudhary,S.		
TITLE	Methods and compositions for synthesis of long chain poly-unsaturated fatty acids in plants		
JOURNAL	Patent: US 6075183-A 1 13-JUN-2000;		
FEATURES	Location/Qualifiers		
source	1..1617		
BASE COUNT	310 a 470 c 410 g 427 t		
ORIGIN	/organism="unknown"		

JOURNAL	Submitted (21-OCT-1996) Nematode Sequencing Project, Sanger Institute, Hinxton, Cambridge CB10 1SA, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rwnematode.wustli.edu			
COMMENT	Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other available information. Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note. For a graphical representation of this sequence and its analysis see:- http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?name=Tl13f2 IMPORTANT: This sequence is not the entire insert of clone Tl13f2. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions. The true left end of clone Tl13f2 is at 1 in this sequence. The true left end of clone W08D2 is at 37953 in this sequence. The start of this sequence (1..104) overlaps with the end of sequence AL022473. The end of this sequence (37953..38060) overlaps with the start of sequence Z70271. IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.			
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Query Match 6.6%; Score 96.2; DB 3; Length 38060;
Best Local Similarity 55.6%; Pred. No. 3.6e-11;
Matches 185; Conservative 0; Mismatches 148; Indels 0; Gaps 0;
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QY 323 tcaattgaaactacgacagagcttccatgatgatgattgaatgaagaatgaaca 382
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QY 383 tatttctgttaagcgatttcaaacactttcaattatggcatttgatttatttctcag 442
DB 35313 TTCTACATTTAGAAAAATCTTGAAACAATCTTCACAATTTCTTTTTCATCTACCTTCAA 35372
QY 443 tatcttggatggtatattacttctgcattgtttattagcacttgcatgagcaacaattcgaa 502
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DB 35433 TGGTTAATCCATGAATTCGCACATCATCATAGTTCTTCANAAACAGATACATATGATTG 35492
QY 563 atttcttcttggtaatttcttacaagga 595
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RESULT 15
AF307940
LOCUS
DEFINITION
Mortierella alpina clone ptMACL-3 delta 6-fatty acid desaturase
mRNA, complete cds.
ACCESSION
AF307940
VERSION
AF307940.1 GI:12007241
KEYWORDS
Mortierella alpina.

ORGANISM Mortierella alpina
Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales;
Mortierellaceae; Mortierella.
REFERENCE 1 (bases 1 to 1374)
AUTHORS King, L., Li, M., Liu, L., Hu, G. and Zhang, L.
TITLE Expression of Mortierella alpina delta 6-fatty acid desaturase gene in Saccharomyce cerevisiae
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1374)
AUTHORS Xing, L., Li, M., Liu, L., Hu, G. and Zhang, L.
TITLE Direct Submission
JOURNAL Submitted (26-SEP-2000) Department of Microbiology, Nankai University, 94 Weijin Road, Tianjin 300071, P.R. China
FEATURES
Location/Qualifiers
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BASE COUNT 266 a 395 c 361 g 352 t
ORIGIN

Query Match 6.2%; Score 90.6; DB 8; Length 1374;
Best Local Similarity 46.8%; Pred. No. 7.6e-10;
Matches 411; Conservative 0; Mismatches 444; Indels 24; Gaps 3;
QY 464 tctgcatgtttattagcacttgcatggaacaattcggatgggttaacacatgagttctgc 523
DB 466 TCGGCTCGCGCTCTTGGGTCTCTTCTGGCAGCAGAGAGATGGTTGGCGCAGACTTTTG 525
QY 524 catcaacagccaacaagaacagacctttgaatgatactattcttctgtcttgtaat 583
DB 526 CACCACAGGCTCTTCAGGACCGCTTTCGGGAGAGACTTTTCGGCGCCCTCTCTTGGGAGGA 585
QY 584 ttctacaaggatttttcaagagattggtggaagcaagcataacacatcatcagctgcc 643
DB 586 GACTGCCAGGGCTTCTCGTCTCATGTTGGGAAGCAAGCAACACATCACCACGCGCC 645
QY 644 acaaatgtaattgatcatgacggtgatatactgacttggcaccacttttcgactttacca 703
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QY 704 ggaagatttgcgaagtataaagccagctttgaaaaagcaat-----tctc 748
DB 706 CATGCTTTTGAGATGTTCTCGGACGTCCTTGACGAGAGCTGACCCGCGATGTGGTCGCGC 765
QY 749 aagattgtaccatatcaacatctctatttcacgcgaatgcttccaatgctccgtttctca 808
DB 766 TTCATGTCCTTAACCCAGACCTGTTCTACTTCCCATTTCTCGTTGGCCGCTCTCCTCC 825
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QY 863 gctatcaaaagaataactcttggagcaagaacaatgttggacattggcgttgggta 922
DB 886 GCCCGTGTGCCCAATTCCTTGGTCGAGCAGCTGCTCTCTGCCATGACACTGGGTAC 945
QY 923 ttctatcaattgttcttattaccacaacatggccact---tcggggtgcttatttcattatt 979

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Db 1126 GGTCTGTGATGTTTCACCTCTGGTCTGTTTCGCCAACTGGTTCACGGGTGGATTGAACCTACCAG 1185
QY 1160 atcgagcacactgttcccaacaatgcacacgttgcaatctgaaatgcttgcgtgaaatat 1219
Db 1186 ATTGACACCACTTGTTCCTTCGATGCCCTCGCCACAACTTTTCAAAAGATCCAGCCTGCT 1245
QY 1220 gtgaaagaatggtgcaaaagagaataatcttacctctgctgatgactacttttgacgga 1279
Db 1246 GTCGAGACCTTGTGCAAAAAGTATGTTCCGATACCCACACACCTGGCATGATCGAGGGA 1305
QY 1280 tatgcaatgaattgcaacaattgaaaaatatggctgag 1318
Db 1306 ACTGCAGAGGCTCTTTAGCCGTTTGAACGAGGTCTCCAAG 1344
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Search completed: August 7, 2002, 02:55:26
Job time: 5057 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 01:39:59 ; Search time 272.14 Seconds
(without alignments)
9223.668 Million cell updates/sec

Title: US-09-555-093-1
Perfect score: 1462
Sequence: 1 gctcaccaaatgtgtcg.....ataaaacctgttttcaa 1462

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802.*
1: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
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23: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1451	99.2	1463	20 AAX76589	Caenorhabditis ele
2	350.4	24.0	1461	21 AAA51232	C. elegans fatty a
3	348.2	23.8	1344	20 AAX86961	C. elegans delta 5
4	112.8	7.7	1275	21 AAA51233	E. gracilis fatty
5	97	6.6	1374	21 AAZ47129	Fungal delta6-des
6	97	6.6	1374	22 AAF25234	Nucleotide sequenc
7	97	6.6	1617	19 AAV63624	CDNA encoding a de
8	97	6.6	1617	20 AAX00889	Mortierella alpina
9	97	6.6	1617	21 AAA09430	M. alpina delta-6

10	76.2	5.2	2012	22	AAF26040	P. patens delta6-d
11	68.4	4.7	1684	19	AAV34398	Borage delta-6 des
12	68.4	4.7	1684	20	AAX24917	Borage delta-6 des
13	68.4	4.7	1685	17	AAT30395	Borage delta-6-des
14	62	4.2	1467	22	AAF25730	C. purpureus delta
15	62	4.2	2040	22	AAF25729	C. purpureus delta
16	58.2	4.0	1471	21	AAAD01349	Florida bitterbush
17	56.2	3.8	1650	21	AAC33846	Arabidopsis thalia
18	56.2	3.8	1650	21	AAC51462	Arabidopsis thalia
19	56.2	3.8	1678	21	AZ44833	A. thaliana sldl D
20	55.8	3.8	2160	22	AAF25734	C. purpureus delta
21	53.6	3.7	1972	21	AAAD01353	Wheat sphingolipid
22	52	3.6	494	19	AAV63634	Phaeodactylum tric
23	52	3.6	494	20	AAX00912	M. alpina desatura
24	52	3.6	494	20	AAV82633	DNA encoding a put
25	52	3.6	494	21	AAAO9444	P. tricornutum fat
26	52	3.6	494	21	AAA14585	DNA encoding a Pha
27	50.2	3.4	1606	21	AAZ44851	Sphingolipid desat
28	47.8	3.3	1934	21	AAAD01352	Soybean sphingolip
29	47.4	3.2	1594	21	AAZ44832	B. napus sldl DNA.
30	47	3.2	1335	22	AAI66599	Rat fatty acid des
31	47	3.2	1335	22	AAI19402	Rat delta-6-desatu
32	46.2	3.2	880	21	AAAD01351	Soybean sphingolip
33	46	3.1	2943	21	AAV70229	Plasmodium falcipa
34	45.8	3.1	82588	21	AAF22301	BAC containing rep
35	45.4	3.1	1082138	21	AAF22305	Arabidopsis thalia
36	45.4	3.1	1335	21	AAA49932	Human delta-5-desa
37	45.4	3.1	1335	22	AAF25236	Nucleotide sequenc
38	45	3.1	451	22	AAH50922	Lipid modification
39	45	3.1	451	22	AAH56909	P patens lipid met
40	45	3.1	451	22	AAH56929	P patens lipid met
41	45	3.1	1465	21	AAAC2244	Arabidopsis thalia
42	44	3.0	347	22	AAF68420	Human lung tumour
43	44	3.0	482	23	AAV74465	DNA encoding novel
44	44	3.0	1478	19	AAV34206	Human secreted pro
45	44	3.0	1700	21	AAZ93706	CYB5RP fatty acid

ALIGNMENTS

RESULT 1

AAX76589
ID AAX76589 standard; cDNA; 1463 BP.

XX

AC AAX76589;

XX

DT 11-AUG-1999 (first entry)

XX

DE Caenorhabditis elegans Delta 6 desaturase Ced6.1 encoding cDNA.

XX

KW Caenorhabditis elegans; C. elegans; Delta 6 desaturase; Ced6.1;

KW gamma-linolenic acid; GLA; plant fatty acid; octadecatetraenoic acid;

KW OTA; eicosanoid; eczema; mastalgia; atherosclerosis; coronary disease;

KW hypercholesterolaemia; diabetic neuropathy; viral infection; acne;

KW hypertension; cirrhosis; cancer; ss.

XX

OS Caenorhabditis elegans.

XX

FH Key Location/Qualifiers

FT CDS 11..1342

FT /*tag= a

XX

PN W09927111-A1.

XX

PD 03-JUN-1999.

XX

PF 24-NOV-1998; 98WO-GB03507.

XX

PR 24-NOV-1997; 97GB-0024783.

XX (UYBR-) UNIV BRISTOL.

XX

PI Napier JA;

WPI; 1999-370905/31.
P-PSDB: AAY17751.

Desaturase enzymes, the genes encoding them and their uses

XX
PS
Claim 29: Fig 1: 44pp: English.

The present sequence encodes *Caenorhabditis elegans* Delta 6 desaturase, designated *Ced6.1*. Desaturase enzymes (I) may be used as immunogens to raise and select antibodies (which may be used in immunassays, and diagnostic tests to detect the presence of (I) in a sample, or to purify (I)) or as a selectable marker for transformation, especially transformations involving plants. (I) can be used to produce gamma-linolenic acid (GLA) (and derivatives of it), which is a high value plant fatty acid that is widely used in medicine for the preparation of compositions for treating disorders associated with deficiencies in GLA or deficiencies in metabolites derived *in vivo* from GLA, such as octadecatetraenoic acid (OTA) and eicosanoids. Disorders that may be treated with GLA and OTA include eczema, mastalgia, atherosclerosis, hypercholesterolaemia, coronary disease, diabetic neuropathy, viral infections, acne, hypertension, cirrhosis and cancer. The nucleotide sequences (II) encoding (I) may be used as probes or primers. Probes may be used to identify and purify nucleic acids and so may be used in diagnosis to detect the presence of (II) in a sample. Primers are useful for amplifying DNA by polymerase chain reaction (PCR). (II) may also be used to prepare an organism that is either chill resistant or that accumulates GLA or metabolites derived from GLA. Hybridizing DNA molecules may be used as anti-sense molecules to alter the expression of (II) by binding to it and preventing transcription. Hybridizing molecules may also be provided as ribozymes which regulate expression by cleaving RNA molecules.

Sequence 1463 BP; 445 A; 288 C; 277 G; 453 T; 0 other;

	Query Match	99.2%	Score 1451;	DB 20;	Length 1463;
	Best Local Similarity	99.9%;	Pred. No. 0;	Mismatches 0;	Indels 1; Gaps 1;
	Matches 1462;	Conservative			
QY	1 gctcaccaaatggtcgtcgacaagaatgcctccgggcttcogaatagaagtcgatggcaa	60			
Db	1 gctcaccaaatggtcgtcgacaagaatgcctccgggcttcogaatagaagtcgatggcaa	60			
QY	61 atggcttaccttagcaggaattcggtagaagaacatccaggagagactgtttattgaaca	120			
Db	61 atggcttaccttagcaggaattcggtagaagaacatccaggagagactgtttattgaaca	120			
QY	121 atalagaanaattcgagtgctactcatattttccacgcctttccacgaagatcttctcaggc	180			
Db	121 atalagaanaattcgagtgctactcatattttccacgcctttccacgaagatcttctcaggc	180			
QY	181 ttataagcaaaattgaccttctgaaaagcagcgagagcaogatgaattcctttgagaaca	240			
Db	181 ttaagaacaattgaccttctgaaaagcagcgagagcaogatgaattcctttgagaaca	240			
QY	241 attggaaaagagaccttgacaaaagtgtataccaattgtatcagcatatgatgtcagttgcc	300			
Db	241 attggaaaagagaccttgacaaaagtgtataccaattgtatcagcatatgatgtcagttgcc	300			
QY	301 acagaagaaagaaatgggtgaatcatttcgaaaaactacgacagaagcttcacatgatcgg	360			
Db	301 acagaagaaagaaatgggtgaatcatttcgaaaaactacgacagaagcttcacatgatcgg	360			
QY	361 attaatgaagcaaatgaaacatatcttcgtttkaaagcgatttcaaacactttcaattat	420			
Db	361 attaatgaagcaaatgaaacatatcttcgtttkaaagcgatttcaaacactttcaattat	420			
QY	421 ggcaattgcatttttatcttccaagtactcttgatgggtatattactctgcatgtttatttagc	480			
Db	421 ggcaattgcatttttatcttccaagtactcttgatgggtatattactctgcatgtttatttagc	480			

RESULT 2

AAA51232

ID AAA51232 standard; cDNA; 1461 BP.

XX

Db 1393 attaatcaattatttttccatgtgttctattcgtgtgttttaattttcc 1444

RESULT 3

AA85961

ID AAX86961 standard; cDNA; 1344 BP.

XX

AC AAX86961;

XX

XX 24-SEP-1999 (first entry)

XX

DE C. elegans delta 5-fatty acid desaturase encoding cDNA.

XX

XX Delta 5-fatty acid desaturase; dihomogamma linolenic acid; gene therapy;
KW arachidonic acid; cholesterol; polyunsaturated fatty acid; foodstuff;
KW dietary supplement; prostaglandin; ss.

XX

OS Caenorhabditis elegans.

XX

XX WO9933958-A2.

XX

XX 08-JUL-1999.

XX

PF 23-DEC-1998; 98WO-GB03895.

XX

XX 29-JUN-1998; 98GB-0014034.

PR

XX 23-DEC-1997; 97GB-0027256.

XX

XX (UYBR-) UNIV BRISTOL.

PA

XX Michaelson L, Napier JA, Stobart K;

PI

XX WPI: 1999-444067/37.

DR

XX P-PSDB; AAY21890.

XX

XX New isolated delta5-fatty acid desaturase enzymes useful in gene

PT therapy

XX

XX Claim 4; Page 21; 36pp; English.

XX

CC The invention provides delta 5-fatty acid desaturases obtained from
CC Mortierella alpina and Caenorhabditis elegans. The delta 5-fatty acid
CC desaturases catalyze the production of polyunsaturated fatty acids, e.g.
CC the conversion of dihomogamma linolenic acid to arachidonic acid. The
CC genes can be used in gene therapy as a preventative treatment, e.g. in
CC patients suffering from high levels of cholesterol or other conditions
CC where administration of polyunsaturated fatty acids may have beneficial
CC disease-preventative effects. The polyunsaturated fatty acids can be used
CC in foodstuffs or dietary supplements. The delta 5-fatty acid desaturases
CC can also be used for the synthesis of prostaglandins or modulation of the
CC synthesis. The products can also be used for detection and diagnosis. The
CC present sequence represents the cDNA encoding the C. elegans delta
CC 5-fatty acid desaturase.

XX

SQ Sequence 1344 BP; 396 A; 269 C; 261 G; 418 T; 0 other;

Query Match 23.8%; Score 348.2; DB 20; Length 1344;
Best Local Similarity 55.8%; Pred. No. 2.4e-74;
Matches 712; Conservative 0; Mismatches 553; Indels 12; Gaps 2;

Qy 44 atgaaggtcgaatggtcctacattgagcaggaatggtgaagaaacatccaggga 103

Db 37 attaaaaattgatgaaatggtgcaaatgacgatgctgctcctgagatcacatccagggt 96

Qy 104 ggaagctgttatgaacatatagaataatcgatgctactcatatatttccacgctttccac 163

Db 97 ggtagtgaattactactacataaaaatgatggtccactacgtattccacacattccat 156

Qy 164 gaagagcttctcaggcttataagcaacttgacctctcgtgaaagacagg-----agag 217

Db 157 actggttctaaagacgtacataatggtcgtgacagaattgaaaaagagtgccctacacaa 216

Qy 218 cacgatgaattcctctgagaacaaattggaaaagagacttgacaaagttgatatacaatgta 277

Db 217 gaaccagagatcccgagattataagagatgacccaatcaaagggaattgatgagtgaacatg 276

Qy 278 tcagcatatgatgtcagtggttgacacaagaaaagaaatggttgaaatcatctcgaaaaacta 337

Db 277 ggaactttcaatattcttgagaacagatctgcccaaaataaataaaagtctcactgatcta 336

Qy 338 cgacagaagcttccatgatgatgattaaatgaagcaaatgaacatatattctctgtttaaa 397

Db 337 cgtatgogagttcgtgcagaaggaccttatggatggatcccttctgtctacattagaaaa 396

Qy 398 gcgatttcaacaccttcaattatggcatttgcattttatcttcagatctcttggtggttat 457

Db 397 attctgaaaacaattctcaaatcttttgcattctacccttcaataccacacatatattat 456

Qy 458 attacttctcatgtttatttagcatttgcattggaacaataatcggaattgaacacatgag 517

Db 457 ctccatcagctatttctaattggagttgctggcaacaattgggatgggttaattccatgaa 516

Qy 518 ttctgccatcaacagccaacaaagaacagaccttggatgatactatttcttcttctt 577

Db 517 ttccacatcctcagttgttcaaaaacagatactacaatgatttggccagctattctgtt 576

Qy 578 ggtaatcttcaagagattttcaagagattggtggaaggacaaagcaataacacatcatcac 637

Db 577 ggaacttttcaagagattctcatctggtggttggaagagcagacacaatgtgcatacac 636

Qy 638 gctgccacaaatgtaattgatcatgaoggtgatcatcgacttggcaccacttttgcacatt 697

Db 637 gcagccacaaatggttggacgagcagagatctgtatttagtcccatctctctgtctaca 696

Qy 698 attccagagagatttgcagatataagccagcttggaaaaagcaaatctcaagatttata 757

Db 697 gtggcagaacatctcaacaattat-----tctcaggattcattgggttactactctatc 750

Qy 758 ccatacaacatctctatttcaccgcgaatgcttccaatgctccgtttctctatggactggt 817

Db 751 agatggcaaatgttcattggacattcatgttaccattctccgtctctctggtctctt 810

Qy 818 cagtcagttcaattgggttattcaagaagaaatcaaatggagtacaaggtctatacaagaat 877

Db 811 cagtcacatcttctgttagtcagatgccactcattattatgactattacagaaataact 870

Qy 878 gcattctgggagcagaacaaatgttgacattggccttgggttattctatcaattgttc 937

Db 871 gcgattatgacaggttggtctctcttgcactggcgttggctcattgggttgcattgtat 930

Qy 938 ttattaccaacatggccacttcgggttcttatttctatttccacaaatgggagagggc 997

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Qy 1118 tctccattcattggtggttgggtggactcaattatcatcagatcgagcaccacttgttc 1177

Db 1111 ggaagattcattgactggttgggaggtcttaactatcagattgagcaccacttttc 1170

Qy 1178 ccaacaatggcaactgtcaatctggtggtgaaatgtgaaagaatggtgcaaa 1237

Db 1171 ccaacgatgcacacacaaacttgaacactgttatgccacttattgagagatttgcagca 1230

Qy 1238 gagaataatctctcctcctcgtcgtgactcatttgcaggtatgcaatgaatttgcga 1297

Db 1231 gcaaatggtttaccatacatagttgcagattatttccacaggtattctggtctgaaatgag 1290

Qy 1298 caattgaaaaatatggc 1314

PI Kopchick JJ, Kelder B, Huang Y, Kirchner SJ, Mukerji P;
XX WPI; 2000-072619/06.
DR P-PSDB; AAF56045.
XX Producing essential fatty acids and long-chain polyunsaturated fatty
PT acids, for use in nutritional, animal feed and medical formulations -
PT Disclosure; Fig 8; 71pp; English.
PS
XX The invention relates to a method of generating novel compositions
CC comprising animal cells producing essential fatty acids (FAs). The animal
CC cells are produced by transforming cells, e.g. embryonic stem cells, with
CC nucleic acid encoding heterologous enzymes involved in fatty acid,
CC e.g. long chain or polyunsaturated fatty acid (PFA) biosynthesis. This
CC sequence is an example of such a nucleic acid sequence and encodes a
CC fungal delta6-desaturase. The essential FAs obtained can be used in
CC nutritional formulations or animal feed formulations. The long chain PFAs
CC can be used in nutritional formulations, cosmetic formulations or animal
CC feed formulations. The products can also be used for producing transgenic
CC animals which can be used for producing essential FAs which can be used
CC for producing downstream products such as leukotrienes, thromboxanes,
CC arachidonic acid, eicosapentaenoic acid or docosahexaenoic acid. The
CC products can also be used in cell culture. The animal or milk fat
CC produced can be administered to treat malnutrition.
XX
SQ Sequence 1374 BP; 257 A; 387 C; 378 G; 352 T; 0 other;

Query Match 6.6%; Score 97; DB 21; Length 1374;
Best Local Similarity 47.2%; Pred. No. 1.le-13;
Matches 415; Conservative 0; Mismatches 440; Indels 24; Gaps 3;

Qy 464 tctgcattgttattagcacttgatgagcaacattcgatggttaacacatgagttctgc 523
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 466 tcggctgcgcttgggtctgtctgagcagtcgagtggtggtcgcagacttttg 525
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 524 catcaacagcaacaaagacactttgatgatactattcttcttcttcttctgta 583
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 526 catcaacaggtcttcagagaccgttctcggtgagttcttctcggtcttctgggaggt 585
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 584 ttcttaacagatttcaagagattggtggaagacaagataacactcaacagctgcc 643
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 586 gtctgcagggctcc 645
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 644 acaaatgtaattgatcatgacgtgagtcacacttggcaccacttttcgatttattcca 703
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 646 cccaacgtccacggcagagatcccgacattgacacccactctgttgactggagtgag 705
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 704 ggagatttgtcaagtataaggccagcttttgaaaaagcaat-----tctc 748
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 706 catgcttgagagattctcgtgagtcctccagatgagggagtcgacccgcatgtggtcgcgt 765
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 749 aagattgtaccatatcaacatctctatttaccgcaatgcttccaaatgctcgtttctca 808
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 766 ttcatggtctcgaacagacatggttttacttccacttctctctctctctctctctcc 825
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 809 tggactgtcagtcagttcaatgggtatt-----caagagaaatcaaatggagacaa 862
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 826 tgggtccctcagtcattctcttctgtctgctacacggtcagggcccaacagccctcgggc 885
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 863 gtctataaagaatgcatctctgggagcaagcaacattgttgacattgggtctgggta 922
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 886 gcgcgttgcccatctctgttgtagagcagctgctgctgtcgatgcactggacctggtag 945
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 923 ttctataaatgttcttattaccacatggccact---tcgggttgcattatttatttatt 979
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 946 ctgcgccacattctctgttcatcaagatcccgctcaacatgctggtgtaatttttggtg 1005
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 980 tcacaaatgggagggccttttattgctcacgtgtagcttccacttccacacataactctgtt 1039
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 1006 tcgcagggcgtgtgcggaaacttctgtgagctgtgttctcgtcacaacacacaggtatg 1065
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||

Qy 1040 gataagtatccagccaattctcgaattttaaacaaacttcgccgctcttcaaatatttgacc 1099
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 1066 cctgtgatctcgaagaggcggtcgatattgatttcttcacgaagcagatcatcag 1125
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 1100 acagcaacatgactccatctccattcattgattggttgggtggactcaattatcag 1159
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 1126 ggtcgtgatctccaccgggtctatttgcacactggttcacgggtggattgaactatcag 1185
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 1160 atcgagcaccactgttctcccaacatgccagttgcaatctgaaatgcttgcgtgaaatat 1219
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 1186 atcgagcaccactgttctccctcgatgctcgcacacttttcaaatcagcagcctgct 1245
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 1220 gtgaagaatggtgcagaagaaataatcttctaccctcgtcgatgactacttttgacgga 1279
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 1246 gtcgagacccgtgcacaaagtacatgtcgcataccacacacccggtgatcgagggga 1305
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 1280 tatgcaatgaatttgcaacaattgaaaaatatggctgag 1318
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 1306 actgcagaggtcttttagcgcgtctgaacgaggtctccaag 1344
Db |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||

RESULT 6
AAF25234
ID AAF25234 standard; DNA; 1374 BP.
XX
AC AAF25234;
XX
DT 30-APR-2001 (first entry)
XX
DE Nucleotide sequence of a fungal delta6 desaturase.
XX
KW delta6 desaturase; desaturase gene; elongase gene; fatty acid;
KW eicosanoid; nutrition; infant formula; dietary supplement;
KW dietary substitute; animal feed; ss.
XX
OS Mortierella alpina.
XX
FH Key Location/Qualifiers
FT CDS 1..1374
FT /*tag= a
FT /product= "delta6 desaturase"
XX
XX WO200104636-A1.
XX 18-JAN-2001.
XX 11-JUL-2000; 2000WO-US19011.
XX 12-JUL-1999; 99US-0351525.
XX (UYOH-) UNIV OHIO.
XX
XX Kopchick JJ, Kelder B;
XX
XX WPI; 2001-182622/18.
XX P-PSDB; AAB31684.
XX
XX New compositions comprising cells that express desaturases and
XX elongases, for synthesizing essential fatty acids or long-chain
XX polyunsaturated fatty acids, used in nutritional, cosmetic or animal
XX feed formulations -
XX
XX Disclosure; Fig 8; 93pp; English.
XX
XX The present sequence encodes a delta6 desaturase. The desaturase
XX polynucleotide sequence was used to trasfect mammalian cells, to
XX produce animal cells expressing a desaturase gene and/or an elongase
XX gene. Compositions comprising cells of the invention are useful for
XX synthesising essential fatty acids, their derivatives or downstream
XX products, as well as altered levels of long-chain polyunsaturated
XX fatty acids and eicosanoids. The compositions are useful in nutritional
XX formulae, e.g. infant formula, dietary supplements or dietary
XX substitutes for both humans and animals. The compositions are also

CC useful in cosmetic or animal feed formulations. Furthermore, the
XX compositions may also be used as fat free media or as research reagents.
SQ Sequence 1374 BP; 257 A; 386 C; 378 G; 353 T; 0 other;

Query Match 6.6%; Score 97; DB 22; Length 1374;
Best Local Similarity 47.2%; Pred. No. 1.1e-13;
Matches 415; Conservative 0; Mismatches 440; Indels 24; Gaps 3;

QY 464 tctgcatgtttattagcacttgagcaaatcggatggttaacacatgattctgc 523
DB 466 tcggctgcgcttttggcttctggcagcagtgctggtggtcactacacttttcg 525
QY 524 catcaacagccaacaaagacagaccttgaatgactattcttcttcttggtaat 583
DB 526 catcaccaggtctccaggaacgcttctgggtgatcttttcggcgcttcttggaggt 585
QY 584 ttcttacaagattttcaagagattggtggaaggacatacaactcatcagctgcc 643
DB 586 gtctgccagggtctctctctctgctggtggaaggacatacaactcaccacgcgc 645
QY 644 acaaatgtaattgatcatgacggtgatctcgacttggcaccacttttcgattttcca 703
DB 646 cccaacgtccacggcggaggtcccacattgacccccctctctgtgacctggagtgag 705
QY 704 ggagatttgcgaagtataagccagctttgaaaaagcaat-----tctc 748
DB 706 catgctgtgagatgttctcggatgtcccgatgagagctgacccgcgtggtcgctg 765
QY 749 aagattgtaccatacaactctctatttccacgcaatgcttccaatgctcgtttctca 808
DB 766 ttcatggtctgaacagacacctggttttacttccccattctctgtttcccgctctcc 825
QY 809 tgactgttcagtcagttcaatgggtatt-----caaaagaaatacaaatgagtaacaag 862
DB 826 tgggtcctccatccattctcttctgtcgtctaacggtcagggcccaacgcccctcgggc 885
QY 863 gtctatcaaaagaatgcattctgggagcaagcaacaattgttgacattgggcttgggta 922
DB 886 gcgctgtgcccattctgttgcagcagctgtcgttgcgatgcactggacctgggtac 945
QY 923 tctatcaattgttcttattaccacatggccact---tcggggtgcttatttcaattatt 979
DB 946 ctgcgcacacatgtctgttctatcaaggaatcccgatcccatgctggtgacttttgggtg 1005
QY 980 tcacaaatggaggagggccttttattgctcagctagtcactttcaaccataactctgtt 1039
DB 1006 tcgcgggcgggtgtgcggaactgttggcgatcgtgttctcgtcacaacacagctatg 1065
QY 1040 gataagatccagccaattctcgaattttaaacacttcgcgctcttcaaattttgacc 1099
DB 1066 cctgtgactcgaaggaggagcggtcgatagtgatttcttcacgaagcagatcatcag 1125
QY 1100 acacgaacatgactccatctccatcatctgattggttgggtggagctcaattatcag 1159
DB 1126 ggtcgtgatgtccaccgggtctatttgcgaactggttcacgggtggtggaactatcag 1185
QY 1160 atcagacaccactgttcccaacaaatgcacgttgcaatctgaatcgttgcgtgaaatat 1219
DB 1186 acagagcaccattgttccctcgtatgctcgcacaaactttcaagaatccagcgtcgt 1245
QY 1220 gtgaagaatggtgcaagagagaataatcttcttaccctcgtcgatgactactttgacgga 1279
DB 1246 gtcgagaccctgtgcaaaagtaaatgtccgataccacacaccggtgatgatcgaaggga 1305
QY 1280 tatgcaatgaattgcaacaattgaaaaatattggttgag 1318
DB 1306 actgcagaggtctttagccgtctgaacgaggtctccaag 1344

RESULT 7
AAV63624

ID AAV63624 standard; cDNA; 1617 BP.
XX AAV63624;
AC
XX
XX
DT 15-FEB-1999 (first entry)
XX
DE cDNA encoding a delta-6 desaturase enzyme.
XX
KW fatty acid; delta-6 desaturase; polyunsaturated fatty acid;
KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;
KW cancer; diabetes; eczema; platelet aggregation; vasodilation;
KW cholesterol level; endometriosis; premenstrual syndrome;
KW myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis;
KW acute respiratory syndrome; hypertension; inflammatory skin disorder; ss.
XX Mortierella alpina.
OS
XX
FH Key Location/Qualifiers
FT 71..1444
FT /*tag= a
FT /product= delta-6 desaturase
XX
XX WO9846763-A1.
PN
XX 22-OCT-1998.
PD
XX 10-APR-1998; 98WO-US07126.
PF
XX 11-APR-1997; 97US-0834655.
PR
XX (ABBO) ABBOTT LAB.
PA (CALJ) CALGENE LLC.
XX
PI Chaudhary S, Huang Y, Knutzon D, Leonard AE, Mukerji P;
PI Thurmond J;
XX
XX WPI; 1998-594582/50.
DR P-PSDB; AAW84137.
XX
XX New isolated fatty acid desaturase enzymes - used for the production
of polyunsaturated fatty acids for use in, e.g. pharmaceutical
compositions, nutritional compositions, cosmetics or animal feed
Claim 1; Fig 3A-E; 165pp; English.
XX
XX The present sequence encodes a Mortierella alpina fatty acid delta-6
desaturase enzyme. The enzyme sequence is used in the methods of
the invention. The specification describes methods for desaturating a
fatty acid and for producing a desaturated fatty acid by expressing
increased levels of a desaturase. The present desaturase is an enzyme
which introduces a double bond carbons 6 and 7 from the carboxyl end of
a fatty acid molecule. The enzyme can be used for desaturating fatty
acids. The enzyme can be used to produce polyunsaturated fatty acids,
which can be used for treating malnutrition, in pharmaceutical
compositions, in cosmetics or in animal feed. The polyunsaturated fatty
acids can be used for treating e.g. restenosis after angioplasty,
inflammation, rheumatoid arthritis, asthma, psoriasis, cancer, diabetes
or eczema or reduce blood pressure. They can also be used to inhibit
platelet aggregation, cause vasodilation, lower cholesterol levels,
inhibit proliferation of vessel wall smooth muscle and fibrous tissue,
reduce or prevent gastro-intestinal bleeding and other side effects
caused by non-steroidal anti-inflammatory drugs, prevent or treat
endometriosis and premenstrual syndrome, treat myalgic encephalomyelitis
and chronic fatigue after viral infections, treat AIDS, multiple
sclerosis, acute respiratory syndrome, hypertension and inflammatory skin
disorders.
XX
SQ Sequence 1617 BP; 310 A; 470 C; 410 G; 427 T; 0 other;

Query Match 6.6%; Score 97; DB 19; Length 1617;
Best Local Similarity 47.2%; Pred. No. 1.2e-13;
Matches 415; Conservative 0; Mismatches 440; Indels 24; Gaps 3;

Qy	464	tctgcatgtttatagcaacttgcatggtggaacaatttcgagatggtttaacacatgagtcttcgc	533
Db	536	tcgctgcgcgttttgggtctgttcttgccagcagtcggtatggttggtccacgactttttg	595
Qy	524	catcaacagccaacaagaacagacacttgaatgatactatttcttggttcttttggtaat	583
Db	596	catcacaggctctccaggacgcttttcgggttgatcttttcggcgocctctctgggaggt	655
Qy	584	ttcttacaaggattttcaagagattggtggaggaacaagcataaacactcatcacgctgc	643
Db	656	gtctgccaggcttctcgtcctcgtgggtggaagacaagacaacactcaccacgcgc	715
Qy	644	acaaatgtaattgatcatgacggtgatatcgacttggcaccacttttgggaattattcca	703
Db	716	cccaacgtccacgcgaggtatccgacattgacccccacctctgtgacctggagtgg	775
Qy	704	ggagatttgtcaagtataaggccagctttgaaaagcaat-----tctc	748
Db	776	catgctgttggagatgtctctcgatgtccagatgaggagctgacccgcagtgtgctgcgt	835
Qy	749	aagattgtaccatatacaatctctatttccacgcaatgcttccaaagtctccgcttctcca	808
Db	836	ttcatggtcctgaaccagaccgtttttactttcccatctctcgtttgcccgtctctcc	895
Qy	809	tggacttggctcagcttccatgctgaat-----caaaagagatcaaatggagtacaag	862
Db	896	tgggtctccagtcceattctcttctgtctgctaaacgctcaggcccaacagccctcggc	955
Qy	863	gtctatcaagaagaatcattcttggagacaagacaacattgttgacattggcttgggta	922
Db	956	gcgcgtgtcccatctcgttgtctgagcagctgtcgtctgcgagtgcactggacctggcac	1015
Qy	923	ttctatcaattgttcttattacaacatggccact---tcgggttgccttatttctatt	979
Db	1016	ctgcaccactgttctgttcatcaaggatccgtccaacatgtcgtgtacttttgggtg	1075
Qy	980	tcacaatatgggaggagcccttttgattgctcagctagtcacttccaaccataactctgtt	1039
Db	1076	tcgcaggcgggtgcggaaacttgttggcgatcgtgtctcgtccaaccacaacggtatg	1135
Qy	1040	gataagtatccagccaattctcgaattttaacaacttcgcgcctcttcaaatttgacc	1099
Db	1136	ccgtgatctcgaaggaggcgggtgatattgatttcttccaagacagatcatcaag	1195
Qy	1100	acacgcaacatgactccatctccattcatttattggtcttgggtggactccaatatcag	1159
Db	1196	ggtcgtgatgccaccgcgggtctatttggcaactggttcacggggtggatgaaactatcag	1255
Qy	1160	atcgagcacacttgttcccaacaatgccagctgcaatctgcaatgcttgcgtgaaatat	1219
Db	1256	atcgagcacacttgttccctctcgatgcctggcgaacttttcaaaagatccagctcgt	1315
Qy	1220	gtgaaagaaatgggtgcaagagaataatcttacttaccctcgtcgatgactactttgacgga	1279
Db	1316	gtcgagacctgtgcaaaaagataaatgtccgataccacacaccgcgttatgatcgaggga	1375
Qy	1280	tatgcaatgaatttgcacaattgaaaaatatggtctgag	1318
Db	1376	actgcagagctctttagcctctctgaacdaggtcttccaa	1414

RESULT

RESULT 0
AAX00889
ID AAX00889 standard; DNA: 1617 BP.

AA
AC
AAX00889:

DT 26-MAR-1999 (first entry)

DE Mortierella alpina delta 6 desaturase encoding DNA.

Delta 6 desaturase; recombinant; fatty acid desaturase; FAD; PUFA; oil; XX KW

polyunsaturated fatty acid; linoleic acid; arachidonic acid; linolenic; stearidonic acid; eicosapentaenoic acid; malnutrition; feeding formula; dietary supplement; prostaglandin; restenosis; angiotlasty; inflammation; rheumatoid arthritis; psoriasis; osteoporosis; cancer; eczema; AIDS; diabetes; cosmetic; animal feed: ss.

Mortierella alpina.

```

Key
CDS
Location/Qualifiers
71..1443
/*tag= a
/product= "delta 6 desaturase"

```

WO9846764-A1.

22-OCT-1998.

10-APR-1998; 98WO-US07421.

24-OCT-1997; 97US-0956985.

11-APR-1997; 97US-0833610;
11-APR-1997; 97US-0834033;

II-APR-1991; 97US-0834655.

(ABBO) ABBOTT LAB.
(CALJ) CALGENE LLC.

Chaudhary S, Huang

1. **Introduction**

WPI; 1999-080739/07;
P-PSDB; AAW95504.

Nucleic aci

practices – useful in therapeutically, e.g.

Claim 1; Fig 3A-

This DNA encodes a Mortierella alpa

nucleotide sequences (AAX00889 to AAX00891) encoding M. alpina

coupled to an expression control sequence functional in prokaryotic cells.

fatty acid desaturase (FAD), can be

containing them are used to produce oils such as linoleic acid, arachidonic acid, gamma-linolenic acid, dihomo-gamma-linolenic acid, stearidonic acid and eicosapentaenoic acid (EPA). These plant oils are used: (i) to treat malnutrition; (ii) in infant feeding formulas, or dietary supplements or substitutes, for use in humans or animals; (iii) for treating disorders associated with inadequate consumption or production of PUFA (or their metabolites such as prostaglandins), e.g. stenosis after angioplasty, inflammation, AIDS, rheumatoid arthritis, psoriasis, osteoporosis, cancer, eczema, diabetes; (iv) as cosmetics, and (v) as animal feeds. Fragments of the DNA are used as probes to isolate related coding sequences. Recombinant plants can produce high yields of PUFA, since new pathways can be created and unwanted ones suppressed. Plants can be engineered to express oils of particular PUFA composition, e.g. one similar to that in human milk, and product recovery is simpler than with e.g. fish.

Sequence 1617 BP; 310 A; 470 C; 410 G; 427 T; 0 other;

Query Match	6.63:	Score 97:	DB 20:	Length 1617:
Query Match	6.63:	Score 97:	DB 20:	Length 1617:

Query Match	0.68;	Score 97;	DB 20;
Best Local Similarity	47.28;	Pred. No. 1.2e-13;	

MACCLES 415; CONSERVATIVE 0; MISNALLIES 440; INDEXES 24; GAPS 3,

Qy 464 tctgcatgtttattagcacttgcatggcaacaattcggatgggttaacacatgagttctgc 523

Db 536 tcggctgcgcttttggggtctgttctggcagcagtcggttggttggtcacgacttttg 595


```
Db 776 catgctgtggagatgtcttcgagatgtccagatgaggagcagaccgcagtggtgcgct 835
Qy 749 aagattgtaccatacaacatctctattaccgcgaatgcttccaaatgctcgtttctca 808
Db 836 ttcatggtctgaaccagacgtggtttacttcccactctctctgttgcgcgtctccc 895
Qy 809 tggactgtgcagtcagtcactcaatgggtatt-----caagagaatcaaatggagtacaag 862
Db 896 tgggtcctccagtcactctctgtgtgctgaacggtcaggcccaacagccctcgggc 955
Qy 863 gtctatcaaaagaatgcatcttgggagcaagaacaatgtttggacattgggctgggta 922
Db 956 ggcgctgtgccatctcgtgtgtcgagcagctgtcgtgtcgatgcactggacctggta 1015
Qy 923 ttctatcaatgtcttattaccacatggccact---tcgggtgtctatttcaattatt 979
Db 1016 ctgcgccacatgtctctgttcatcaagatcccgctcaacatgctgtgttacttttgg 1075
Qy 980 tcacaaatggaggagcgttttattgtctcacgtagtcactttcaaccataaactctgt 1039
Db 1076 tcgcagcggtgtgcgaaactgtgtgcgacgtgtgtctcgtcaacacacacaggtatg 1135
Qy 1040 gataagtatccagccaatctctogaatttaaacacttcgcgcgtcttcaaattttgacc 1099
Db 1136 cctgtgatctcgaaggaggcgtgtgatgtgattcttcacgaagcagatcatcacg 1195
Qy 1100 acagcaacatgactccatctccattcattgattgctcagctagtcactttcaaccataaactctgt 1159
Db 1196 ggtcgtgatgtccacccgggtctatttcccaactgggttcacgggtggattgaactatcag 1255
Qy 1160 atcgagcaccactgttcccacaacatgcacgttgcaatctgaaatgcttgcgtgaaatat 1219
Db 1256 atcgagcaccactgttcccttcgactgctgcgcacaactttcaaatccagcctgct 1315
Qy 1220 gtgaagaatggtgcgaagagaataatcttcttaccctcgtcgtgatctattttgacgga 1279
Db 1316 gtcgagaccctgtgcgaagataatgtccgataccacaccaccggtgatgatgagga 1375
Qy 1280 tatgcaaatgattgcaacaattgaaaaaatatgctgag 1318
Db 1376 actgcagaggctcttagcgtctggaacgaggtctccaag 1414

RESULT 10
AAF26040
ID AAF26040 standard; cDNA; 2012 BP.
XX
AC AAF26040;
XX
DT 23-APR-2001 (first entry)
XX
DE P. patens delta6-desaturase cDNA.
XX
KW Delta6-desaturase; unsaturated fatty acid; transgenic; oil; lipid;
KW fatty acid; human nutrition; animal nutrition; cosmetic; pharmaceutical;
KW agricultural chemical; ds.
XX
OS Physcomitrella patens.
XX
FH Key Location/Qualifiers
FT CDS 319..1896
FT FT /*tag= a
FT FT /product= "delta6-desaturase"
XX
FN WO200102591-A1.
XX
PD 11-JAN-2001.
XX
PF 04-JUL-2000; 2000WO-EP06223.
XX
PR 06-JUL-1999; 99US-0347531.
PR 30-JUN-2000; 2000DE-1030976.
```

```
XX
PA (BADI ) BASF AG.
XX
PI Heinz E, Girke T, Scheffler J, Da Costa Silva EO;
XX
DR WPI; 2001-123117/13.
DR P-PSDB; AAB46810.
XX
PT Production of unsaturated fatty acids, useful e.g. in nutrition,
PT cosmetics or pharmaceuticals, in organisms transformed with
PT Physcomitrella patens delta-6-desaturase nucleic acid -
XX
PS Claim 1a; Page 38-41; 49pp; German.
XX
CC This invention describes a novel preparation of unsaturated fatty acids
CC (I) by introducing into an organism at least one isolated nucleic acid
CC (II) that encodes a polypeptide (III) with delta6-desaturase activity.
CC Organisms that contain at least 1 wt.% (I), on total fatty acid content,
CC are then selected. (II) is selected from: (a) a 2012 bp sequence (S1),
CC defined in the specification, or its equivalents within the degeneracy of
CC the genetic code; or (b) derivatives of the sequence of (a) that encode a
CC 525 amino acid polypeptide (S2), defined in the specification, or a
CC polypeptide with at least 50% homology with (S2) and practically the same
CC enzymatic activity. The invention also describes (1) transgenic organisms
CC that contain (II); and (2) oils, lipids and fatty acids produced by the
CC new method. The oils, lipids and fatty acids produced by the transformed
CC organisms are used in human or animal nutrition, cosmetics,
CC pharmaceuticals and agricultural chemicals. (III) can also be used, in
CC vitro, for increasing the (I) content of triglycerides. The transgenic
CC organisms have increased contents of (I), or of (i)-containing
CC triglycerides, particularly of gamma-linolenic acid.
XX
SQ Sequence 2012 BP; 482 A; 427 C; 553 G; 550 T; 0 other;

Query Match 5.2%; Score 76.2; DB 22; Length 2012;
Best Local Similarity 56.6%; Pred. NO. 1.3e-08;
Matches 141; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

Qy 412 ttcaattatggcattgcatatttattcttcagtatcttggatggtatattacttctgcagt 471
Db 978 tgcgacgcatgcaataatattgttgagcaagactatttcacggttttggcttcagcttg 1037
Qy 472 ttattagcacttgcatggcaacattcggatggttaacacatgattctgcctcaaca 531
Db 1038 tatgatggtctgtgtttccaaacagtcggtgctatccccatgattttccacaatca 1097
Qy 532 gccacaagaacagacaccttgaatgatactatttcttcttcttggtaatttttaca 591
Db 1098 ggtgttgagacacgctggttaataagttgtcgggtatgtatgcggcaacgcgcttct 1157
Qy 592 aggattttcaagagattggtggaaggaacagcaataacactcatcagctgcacaaatgt 651
Db 1158 ggggttttagtcaggggtggtggaaggaagcaataacacttcatcatgctgtccaaatga 1217
Qy 652 aattgatca 660
Db 1218 atgcgatca 1226

RESULT 11
AAV34398
ID AAV34398 standard; DNA; 1684 BP.
XX
AC AAV34398;
XX
DT 02-MAR-1999 (first entry)
XX
DE Borage delta-6 desaturase gene.
XX
KW Upstream region; regulatory region; sunflower; albumin; seed; expression;
KW lipid metabolism; delta-6 desaturase; transgenic plant; ds.
XX
```


Query Match		4.7%;	Score 68.4;	DB 17;	Length 1685;
Best Local Similarity		44.2%;	Pred. No. 9.5e-07;		
Matches 423;		Conservative	0;	Mismatches 526;	Indels 9; Gaps 3;
QY	381	catatttctgtttaaagcgatttcaacacttccaattatgcatgacattgcatatttattcttc	440		
Db	387	caactttgtctttatagcaatgcttggctatgagttttatggggtttgtttgtg	446		
QY	441	agtatcttggtatattactctgcattgtttattagcaacttgcatacaaatcg	500		
Db	447	aggggtttgtgtacattttgttctgggtgtgttgatgggtttctttggattcagagtg	506		
QY	501	gatgttaacacatgatttctgocatacagcccaacaaagacagacctttgaaatgata	560		
Db	507	gttgattggacatgatgctggcattatattgtagtctgtattcaaggcttaataagt	566		
QY	561	ctattttctgtttgttaattcttacaaggattttcaagagatttgggtgaagaca	620		
Db	567	ttatgggtattttgtgctcaaatgtcttccaggaaataagattgttgggtgaatgga	626		
QY	621	agcataaactcatcagctgcacaaatgtaattgatcatgacggtgatctgacttgg	680		
Db	627	accataatgcacatcactgctgtaataagcttgaaatgacctgtattacaatata	686		
QY	681	caccactttctgcatatttaccagagatttgcgaagtataaggccagctttgaaaaag	740		
Db	687	taccattcttgtgtctccaagttttttggttcactcacctctcatcttctatgaga	746		
QY	741	caattctcaagatttacatatcaacatctctatttaccgcgaatgcttc---caatgc	797		
Db	747	aaaggttgactttgactctttatcaagattctttgtaagtattcaacattggacattt	806		
QY	798	tcggtttctcagctgctcagtcagttcaatgggtattcaaaagagaatcaaatggagt	857		
Db	807	accttatatgtgctgtagctcaaatatgtatgtacaaatctctcataaagtgtttga	866		
QY	858	acaaggtctatcaagaataatgcatctctgtggagcaagcaacaattgttgacattgggctt	917		
Db	867	ccaagagaaatgtctctatagctcaggaactctgtgggtgctagtggtctcgattt	926		
QY	918	gggtattctcaaatgtttctattaccaaatggccacttgggttgcattttcatia	977		
Db	927	ggatcccggtgtgtttcttctgttgcctaatgtgggtgaaagaattatgtttgttttg	986		
QY	978	tttcaaaatgggagggcccttttgattgctcaogtagtcactttcaaccataactctg	1037		
Db	987	caagttatcagtgactggaatgcacaagtcca---gttctcttgaaccactctctt	1043		
QY	1038	ttgataagttaccagccaattctcgaattttaacaaacttcgccgtcttcaaatttga	1097		
Db	1044	caagtgtttatgttgaaagcct---aaagggaataattggtttgagaaacaacggatg	1100		
QY	1098	ccacagcaacatgactcactccattcattcattgattgctttgggtggactcaattatc	1157		
Db	1101	ggactatgacattctctgctctcttggatggattgttctatggtgattgcaattcc	1160		
QY	1158	agatgagcacacactgtttcccaacaaatgccacgttgcaatctgaatgcttcgtgaaat	1217		
Db	1161	aaattgagcatatttttcccaagatcctagatgcaaccttaggaaatctcgccct	1220		
QY	1218	atgtgaagaatggttgcagaagaataatcttcttaccctctgcactgactattgacg	1277		
Db	1221	acgtgatcgagttagcaagaacaataatttgccttacaattatgcatctttctccaagg	1280		
QY	1278	gatatgcaatgatttgacaacattgaaaaaatatggctgagcacattcaagctaaagc	1335		
Db	1281	ccaatgaaatgacatcgaacattgaggaacacagcattgagcaggtaggatataac	1338		

RESULT 14

AAF25730

ID AAF25730 standard; DNA; 1467 BP.

XX	AAF25730;				
AC	06-APR-2001 (first entry)				
XX	C. purpureus delta6-acetylenase/delta6-desaturase DNA SEQ ID NO 3.				
DT	Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;				
XX	transgenic plant; plant oil; triglyceride; nutrition; animal feed;				
KW	cosmetic; ds.				
KW					
XX	Ceratodon purpureus.				
OS					
XX					
FH	Key	Location/Qualifiers			
FT	CDS	10..1461			
FT		/*tag= a			
FT		/product= "delta6-acetylenase/delta6-desaturase"			
XX	WO200075341-A1.				
PN					
XX	14-DEC-2000.				
PD					
XX	07-JUN-2000; 2000WO-EP05274.				
PF					
XX	07-JUN-1999; 99DE-1025718.				
PR	22-DEC-1999; 99DE-1062409.				
PR					
XX	(BADI) BASF AG.				
PA					
XX					
PI	Heinz E, Stymne S, Lee M, Girke T, Sperling P, Zaehringer U;				
XX	WPI; 2001-112150/12.				
DR	P-PSDB; AAB46436.				
DR					
XX					
XX	Nucleic acid encoding delta6-acetylenase or desaturase, useful for				
PT	producing plant oils with increased content of unsaturated fatty acids				
PT					
XX					
XX	Claim 1a; Page 46-48; 69pp; German.				
PS					
XX					
CC	This invention describes a novel isolated nucleic acid (I) encoding				
CC	polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase				
CC	activity. The invention also describes (a) amino acid sequences encoded				
CC	by (I); (b) an expression cassette (EC) containing (I) linked to one or				
CC	more regulatory sequences; (c) a vector containing (I) and EC; (d)				
CC	organisms containing (I), EC or the vectors of (c); (e) preparation of				
CC	unsaturated fatty acids (A) or triglycerides (TG) with increased content				
CC	of (A) by introducing (I) or EC into an oil-producing organism; (f)				
CC	proteins (IIa) of 172 aa or 178 aa (given in the specification); (g)				
CC	production of (A) or TG by using (Ia); and (h) (A) and TG produced by				
CC	method (g). (I) are used to produce transgenic plants (or other				
CC	organisms) that produce oils or triglycerides (TG) with increased content				
CC	of unsaturated fatty acids (A) and to isolate related sequences by				
CC	homology screening. (A), or TG containing them, are useful in human				
CC	nutrition (e.g. infant foods), animal feeds, pharmaceuticals and				
CC	cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes,				
CC	can be used to suppress expression of (II), resulting in oils with				
CC	increased content of saturated fatty acids.				
XX					
SQ	Sequence 1467 BP; 356 A; 349 C; 379 G; 383 T; 0 other;				
	Query Match	4.2%;	Score 62; DB 22; Length 1467;		
	Best Local Similarity	44.0%;	Pred. No. 3.2e-05;		
	Matches 376; Conservative	0; Mismatches 460; Indels 18; Gaps 2;			
QY	464	tttgcatgtttatagcaacttgcacaaattcggttggttaacacatgattctgc	523		
Db	595	tcagccagtttgatgggtctcttcgtccacagtggtggtggtcccatgatttcctt	654		
QY	524	catcaacagcccaacaaagacagaccttgaatgatactattctttgttttggtaat	583		
Db	655	catcaacaggtctttgagaacccgtaccgcgaactcttcttcttggctattttcggaat	714		

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OM protein - protein search, using sw model

Run on: August 6, 2002, 16:04:11 ; Search time 31.81 Seconds
(without alignments)
1546.862 Million cell updates/sec

Title: US-09-555-093-2
Perfect score: 2410
Sequence: 1 MVVDKNASGLRMKVDGKWL.....YAMNLOOLKNMAEHIOAKAA 443

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802.*
1: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
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20: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2410	100.0	443	20 AAY17751	Caenorhabditis ele
2	2382	98.8	473	21 AAY51353	Protein b5cae with
3	1092.5	45.3	447	20 AAY21891	C. elegans delta 5
4	1092.5	45.3	447	21 AAY96721	C. elegans fatty a
5	1079	44.8	454	21 AAY51355	Protein 25bce with
6	597.5	24.8	422	21 AAY96722	E. gracilis fatty
7	592	24.6	520	22 AAB46440	C. purpureus delta
8	590.5	24.5	525	21 AAY51354	Protein b5pp with
9	590.5	24.5	525	22 AAB46810	P. patens delta6-d
10	559	23.2	483	22 AAB46435	C. purpureus delta
11	559	23.2	483	22 AAB46436	C. purpureus delta

12	557	23.1	457	19 AAW84137	A delta-6 desatura
13	557	23.1	457	20 AAW95504	Mortierella alpina
14	557	23.1	457	21 AAY92599	M. alpina delta-6
15	557	23.1	457	21 AAY56045	Fungal delta6-des
16	557	23.1	457	22 AAB31684	Anino acid sequenc
17	555	23.0	457	20 AAW85121	A delta-6 desatura
18	501	20.8	355	19 AAW84139	Desaturase enzyme
19	463.5	19.2	449	21 AAG29290	Arabidopsis thalia
20	462.5	19.2	462	21 AAY71552	Corn sphingolipid
21	460.5	19.1	458	21 AAY51348	Sphingolipid desat
22	460	19.1	448	21 AAY71551	Florida bitterbush
23	456.5	18.9	446	20 AAW85122	A delta-6 desatura
24	454.5	18.9	448	17 AAR98455	Borage delta-6-des
25	454.5	18.9	448	19 AAW67471	Borage delta-6 des
26	454.5	18.9	448	20 AAW98130	Sunflower HADES pr
27	454.5	18.9	448	21 AAY51349	Wheat sphingolipid
28	450.5	18.7	469	21 AAY71555	B. napus sld1 prot
29	443.5	18.4	449	21 AAY51333	Arabidopsis thalia
30	434	18.0	449	21 AAG07392	Arabidopsis thalia
31	434	18.0	517	21 AAG07391	Arabidopsis thalia
32	433	18.0	449	21 AAG53861	Arabidopsis thalia
33	433	18.0	449	21 AAY51334	A. thaliana sld1 p
34	418	17.3	450	21 AAY71554	Soybean sphingolip
35	412	17.1	87	19 AAW84144	Desaturase enzyme
36	411	17.1	444	21 AAY95445	Human delta-5-des
37	411	17.1	444	22 AAB31686	Amino acid sequenc
38	411	17.1	501	22 AAM93314	Human polypeptide,
39	410.5	17.0	326	21 AAG29291	Arabidopsis thalia
40	406	16.8	425	22 AAM25725	Human protein sequ
41	406	16.8	444	21 AAY97538	Human fatty acid d
42	406	16.8	444	22 AAB94041	Human protein sequ
43	398	16.5	432	21 AAY95446	Human delta-5-des
44	398	16.5	746	19 AAW84156	Human desaturase e
45	398	16.5	746	20 AAW85135	A desaturase enzym

ALIGNMENTS

RESULT 1
AAY17751
ID AAY17751 standard; Protein; 443 AA.
XX
AC AAY17751;
XX
DT 11-AUG-1999 (first entry)
XX
DE Caenorhabditis elegans Delta 6 desaturase Ced6.1.

XX
KW Caenorhabditis elegans; C. elegans; Delta 6 desaturase; Ced6.1;
KW gamma-linolenic acid; GLA; plant fatty acid; octadecatetraenoic acid;
KW OTA; eicosanoid; eczema; mastalgia; atherosclerosis; coronary disease;
KW hypercholesterolaemia; diabetic neuropathy; viral infection; acne;
KW hypertension; cirrhosis; cancer.

XX
OS Caenorhabditis elegans.

XX
PN WO9927111-A1.

XX
PD 03-JUN-1999.

XX
PF 24-NOV-1998; 98WO-GB03507.

XX
PR 24-NOV-1997; 97GB-0024783.

XX
PA (UYBR-) UNIV BRISTOL.

XX
PI Napier JA;

XX
DR WPI; 1999-370905/31.

XX
DR N-PSDB; AAX76589.

XX
PT Desaturase enzymes, the genes encoding them and their uses

XX PS Claim 1; Fig 1; 44pp; English.

XX CC The present sequence is *Caenorhabditis elegans* Delta 6 desaturase,

CC CC designated Ccd6.1. Desaturase enzymes (I) may be used as immunogens to

CC CC raise and select antibodies (which may be used in immunoassays, and

CC CC diagnostic tests to detect the presence of (I) in a sample, or to purify

CC CC (II) or as a selectable marker for transformation, especially

CC CC transformations involving plants. (I) can be used to produce gamma-

CC CC linolenic acid (GLA) (and derivatives of it), which is a high value

CC CC plant fatty acid that is widely used in medicine for the preparation of

CC CC compositions for treating disorders associated with deficiencies in GLA

CC CC or deficiencies in metabolites derived *in vivo* from GLA, such as

CC CC octadecatrienoic acid (OTA) and eicosanoids. Disorders that may be

CC CC treated with GLA and OTA include eczema, mastalgia, atherosclerosis,

CC CC hypercholesterolaemia, coronary disease, diabetic neuropathy, viral

CC CC infections, acne, hypertension, cirrhosis and cancer. The nucleotide

CC CC sequences (II) encoding (I) may be used as probes or primers. Probes may

CC CC be used to identify and purify nucleic acids and so may be used in

CC CC diagnosis to detect the presence of (II) in a sample. Primers are useful

CC CC for amplifying DNA by polymerase chain reaction (PCR). (II) may also be

CC CC used to prepare an organism that is either chill resistant or that

CC CC accumulates GLA or metabolites derived from GLA. Hybridizing DNA

CC CC molecules may be used as anti-sense molecules to alter the expression of

CC CC (II) by binding to it and preventing transcription. Hybridizing

CC CC molecules may also be provided as ribozymes which regulate expression by

CC CC cleaving RNA molecules.

XX CC Sequence 443 AA;

Query Match 100.0%; Score 2410; DB 20; Length 443;
Best Local Similarity 100.0%; Pred. No. 1.7e-229;
Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVVDKNASGLRMKVDGKWLILSEELVKKHGPGAVTEQYRNSDATHIFHAFHEGSSQAYKK 60
Db 1 mvvdknasglrmkvdgkwlyiseelvkhhpggavieqyrnsdathifhafhegssqaykq 60

Qy 61 LDLLKKHGEHDEFLEKQLEKRLDKVDINVSAYDVSVAQEKWVSFEKRLKLDHDDGLMK 120
Db 61 ldllkkhgeheflekqlekrldkvdlnvsaydvsavagkwmvsefekrlklhddglimk 120

Qy 121 ANETYFLFKALSTLSIMAFYLYGLWYITSACLLALAWQOFGWLTHFCHQOQPTKNRP 180
Db 121 anetyflfkaltlsimafalylyglwytisacillalawqgfgwlthefchqgptknrp 180

Qy 181 LNDTISLFFGNFLOGFSRDWKKDKHNTHTHAATNVLDHGDIDLAPLFAFIPGDLCKYKAS 240
Db 181 lndtislffgnlfgfsrdwkkdkhnthtaantnvldhgdldlaplfafipgdlckykas 240

Qy 241 FEKATLKTVPYOHLYFTAMLPLRFSTWQSGVQWVFKENQMEYKVYORNAFEGQATIVGH 300
Db 241 fekalikivpyqhllyftamlplrfstwgsgvqvwvfkengmeykvyrnatweqativgh 300

Qy 301 WAWFYQLFLPTWPLRVAYFIISQMGGLLTAHVVTFNHNSVDKYPANSRILNFAALQ 360
Db 301 wawrfyqlflptwplrvayfiisqmgglliahvvtfnhnsvdkypansrilmnfaalq 360

Qy 361 ILTRNTPSPFDIMLWGLNLYQTEHHUFLPTMPRCNLNACVYKWECKENNLPLYVDY 420
Db 361 llttrntpspfdimlwglnglyqtehhflptmprcnlnacvkvkewckennlplyvddy 420

Qy 421 FDGYAMNLIQQLKMAEHIOAKAA 443
Db 421 fdgyamnlqqikmaehioakaa 443

RESULT 2
AAV51353
ID AAV51353 standard; Protein; 473 AA.
XX
AC AAV51353;

XX 27-APR-2000 (first entry)

XX DE Protein b5cae with delta6 fatty acid desaturase activity.

XX KW Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid;

XX KW transgenic plant; crop plant; delta-8-unsaturated long-chain base;

XX KW tolerance; resistance; soil salinity; ion stress; toxicity; drought;

XX KW cold; frost; phytopathogenic microorganism; flowering time; cosmetic;

XX KW pharmaceutical; food; chemical raw material.

XX OS Unidentified.

XX PN DE19828850-A1.

XX PD 30-DEC-1999.

XX PF 27-JUN-1998; 98DE-1028850.

XX PR 27-JUN-1998; 98DE-1028850.

XX PA (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.

XX XX Heinz E, Zaehrer U, Schmidt H, Sperling P;

XX DR WPI; 2000-127549/12.

XX PT New sphingolipid desaturase that selectively introduces double bond

XX PT into sphingolipids and capnoids -

XX PS Disclosure; Page 38-39; 62pp; German.

XX CC This invention describes a novel sphingolipid desaturase that selectively

CC CC introduces a double bond into the sphingobase of the ceramide residue of

CC CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid

CC CC desaturase, or a vector containing the DNA sequence, can be used to

CC CC produce transgenic plants, especially crop plants, with an increased or

CC CC decreased delta-8-unsaturated long-chain base content or an altered

CC CC delta-8-unsaturated long-chain base cis/trans ratio, especially to

CC CC compensate for a delta-8-unsaturated long-chain base deficiency, to

CC CC exclude production of delta-8-unsaturated bases, to increase tolerance

CC CC or resistance to soil salinity, ion stress or toxicity, drought, wet

CC CC conditions, cold or frost and/or phytopathogenic microorganisms, or to

CC CC alter size growth and flowering time. Cells, transgenic organisms or

CC CC plants containing the DNA sequence can be used to produce sphingolipids

CC CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids

CC CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw

CC CC materials. This sequence represents a protein which has delta6 fatty acid

CC CC desaturase activity which is described in the method of the invention.

XX SQ Sequence 473 AA;

Query Match 98.8%; Score 2382; DB 21; Length 473;
Best Local Similarity 93.4%; Pred. No. 1.1e-226;
Matches 442; Conservative 1; Mismatches 0; Indels 30; Gaps 1;

Qy 1 MVVDKNASGLRMKVDGKWLILSEELVKKHGPGAVTEQ----- 37
Db 1 mvvdknasglrmkvdgkwlyiseelvkhhpggavieqysiplnknietrgrgsn 60

Qy 38 -----YRNSDATHIFHAFHEGSSQAYKQLDLLKKHGEHDEFLEKQLEKRLDKVDINVS 90
Db 61 aldilyfyrrnsdathifhafhegssqaykqldllkkhgeheflekqlekrldkvdins 120

Qy 91 AYDVSVAQEKWVSFEKRLKLDHDDGLMKANETYFLFKALSTLSIMAFYLYGLWYI 150
Db 121 aydvsvaqekwmvsefekrlklhddglimkanetyflfkaltlsimafalylyglwyi 180

Qy 151 TSACLLALAWQOFGWLTHFCHQOQPTKNRPLNDTISLFFGNFLOGFSRDWKKDKHNTHTHA 210
Db 181 tsacillalawqgfgwlthefchqgptknrplndtislffgnlfgfsrdwkkdkhnthta 240

QY 211 ATNVIDHGDIDLAFAPFIPGDLCKYKASFEKAILKIVPYOHLXYFTAMPLMLRFSWTGQ 270
Db 241 atnvldhgdldlplafapfipgdlckykasfekailkivpyghlyftamplmlrfswtgq 300
QY 271 SVQWVFKEOMEYKYVQORNAFWEQATIVCHWAWVFOLELLPTWPLRVAYFIISOMGGCL 330
Db 301 svqwvfkenomeykyvqrnatweqatlvghwawvfyqiflptwplrvayfiisqmggsl 360
QY 331 LIAHVVTFNHNSVDKYPANSRIINFAALQILTTNRNMTSPSPIDWLGGLNYQIEHHLFP 390
Db 361 liahvvtnhnsvdkypansriinfaalqiltnrnmtpspfidwlgglngyqiehhlf 420
QY 391 TPNRCNLNACVYVKEWKENMLPYLVDYDFGYAMNLOQLKMAEHIOAKAA 443
Db 421 tprcnlnacmkvkwckennlpylvddyfdgyamnlqqlkmaehioakaa 473

RESULT 3
AAY21891
ID AAY21891 standard; Protein; 447 AA.
XX
AC AAY21891;
XX
DT 24-SEP-1999 (first entry)
XX
DE C. elegans delta 5-fatty acid desaturase.
XX
KW Delta 5-fatty acid desaturase; dihomogamma linolenic acid; gene therapy;
KW arachidonic acid; cholesterol; polyunsaturated fatty acid; foodstuff;
KW dietary supplement; prostaglandin.
XX
OS Caenorhabditis elegans.
XX
PN WO9933958-A2.
XX
PD 08-JUL-1999.
XX
PF 23-DEC-1998; 98WO-GB03895.
XX
PR 29-JUN-1998; 98GB-0014034.
XX
PR 23-DEC-1997; 97GB-0027256.
XX
PA (UYBR-) UNIV BRISTOL.
XX
PI Michaelson L, Napier JA, Stobart K;
XX
DR WPI; 1999-444067/37.
XX
DR N-PSDB; AAX86961.
XX
PT New isolated delta5-fatty acid desaturase enzymes useful in gene
XX therapy
XX
PS Claim 18; Page 23; 36pp; English.
XX
CC The invention provides delta 5-fatty acid desaturases obtained from
CC Mortierella alpina and Caenorhabditis elegans. The Delta 5-fatty acid
CC desaturases catalyze the production of polyunsaturated fatty acids, e.g.
CC the conversion of dihomogamma linolenic acid to arachidonic acid. The
CC genes can be used in gene therapy as a preventative treatment, e.g. in
CC patients suffering from high levels of cholesterol or other conditions
CC where administration of polyunsaturated fatty acids may have beneficial
CC disease-preventative effects. The polyunsaturated fatty acids can be used
CC in foodstuffs or dietary supplements. The Delta 5-fatty acid desaturases
CC can also be used for the synthesis of prostaglandins or modulation of the
CC synthesis. The products can also be used for detection and diagnosis. The
CC present sequence represents the C. elegans delta 5-fatty acid desaturase.
XX
SQ Sequence 447 AA;

Query Match 45.3%; Score 1092.5; DB 20; Length 447;
Best Local Similarity 46.3%; Pred. No. 3.2e-99;
Matches 201; Conservative 84; Mismatches 140; Indels 9; Gaps 4;

QY 12 MKVDGKWLYSBELYKKHGGAVIEQYRNSDATHIFHAFHEGSSQAYKOLDLLKKHGEHD 71
Db 13 ikidgkwqlddavrshpggsaittykmdattvfthtgtskeayqwtelkkeepcq 72
QY 72 E----FLEKQLERKLDKVDINVSAYDVSAQEKKMWSEFEKLKQKLHDDGLMKANETTEL 127
Db 73 epeipdikdpikgid--dvnmgtfniseksaqinkstfdirmrvaeglmndgspfyi 130
QY 128 FKAISTLSIMAFAYLOYLGWVITTSACLLALAWQOQFGLTTFEFCHOQPTKRNPLNDTISL 187
Db 131 rkiletifilfafylyqhtyylpsailingvawqqlgwlihefahqqlfknryyndlasy 190
QY 188 FFCNFIQGSRDWKKDKHNTTHAATNVIDDGDIDIDLAPLFAFIPGDLCKYKASFEKAILK 247
Db 191 fvgnflqgfsqgwkqehnhvhaatnvvgrdgdldlvfyatvaehlhny--sqdswvmt 248
QY 248 IVPYQHLIETAMPLMLRFSWTGQSVQWVFKENOMEYKYVQORNAFWEQATIVGHWAWVYQ 307
Db 249 ifrwghvhwfmlpflrlslwllqslifvsqmpthyydyrntaiyeqvglsihwawslqg 308
QY 308 LFLPTWPLRVAYFIISOMGGGLLIAHVVTFNHNSVDKYPANSRIINFAALQILTRNM 367
Db 309 lyflpdwstrimflvshlvvgfllshvvtfnhysvekfalssninsnyaciqimtrnm 368
QY 368 TPSPFIDWLGGLNYQIEHHLFPTMPRCNLNACVYVKEWKENMLPYLVDYDFGYAMN 427
Db 369 rprfrldwlgglngyqiehhlfptmprhnlntvmpivkfeaaangipymvddyftgfwie 428
QY 428 LOQLKMAEHIOAK 441
Db 429 iegfirnia-nvaak 441

RESULT 4
AAY96721
ID AAY96721 standard; Protein; 447 AA.
XX
AC AAY96721;
XX
DT 26-SEP-2000 (first entry)
XX
DE C. elegans fatty acid delta-5-desaturase.
XX
KW Fatty acid delta-5 desaturase; polyunsaturated; oil; seed;
KW infant formula; dietary supplement.
XX
OS Caenorhabditis elegans.
XX
PN WO200034439-A1.
XX
PD 15-JUN-2000.
XX
PF 06-DEC-1999; 99WO-US28655.
XX
PR 07-DEC-1998; 98US-0111301.
XX
PA (UNIW) UNIV WASHINGTON STATE RES FOUND.
XX
PI Browse JA, Wallis JG, Watts JL;
XX WPI; 2000-431293/37.
XX DR N-PSDB; AAA51232.
XX
PT Purified protein having desaturase activity, useful for creating a
XX double-bond between two carbons
XX
PS Claim 3; Fig 6A; 74pp; English.
XX
CC This is the Caenorhabditis elegans fatty acid delta-5 desaturase. The
CC cDNA sequence is useful for recombinant production of the enzyme and for
CC generating transformed host cells and transgenic plants. The desaturase
CC can be used for creating a double-bond between two carbons. In

CC particular, the enzyme is useful for producing polyunsaturated fatty
CC acids and for generating enzyme-specific antibodies useful for
CC identifying desaturases. Oil-seed plants may be engineered to incorporate
CC the enzyme, so that the plants produce seed oil rich in fatty acids. The
CC fatty acids could be incorporated usefully into infant formula, foods of
CC all kinds, dietary supplements, nutraceutical and pharmaceutical
CC formulations.

XX Sequence 447 AA;

Query Match 45.3%; Score 1092.5; DB 21; Length 447;
Best Local Similarity 46.3%; Pred. No. 3.2e-99;
Matches 201; Conservative 84; Mismatches 140; Indels 9; Gaps 4;

Qy 12 MKVDCGKWLVLSEELVKKPGGAVIEQYRNSDATHIFAFHEGSSQAYKQLDLLKKHGEHD 71
Db 13 ikidgkwcqiddavlrshpggsaittykmdattvfhfhtgskayqwltekkceptq 72
Qy 72 E----FLEKQLEKRLDKVDINVSAYDVSVAQEKKMVESFEKLRQKLDHDDGLMKANETVFL 127
Db 73 epeipdkddpikgid--dvnmgtfnisekrsaqinksfldlrnvraegldmgsplfyi 130
Qy 128 FKAISTLSIMAFYQLVGLWYITTSACLLALAWQFGWLTHFCHQOPTKRNPLNDTISL 187
Db 131 rkiletifilfaylqlyhtyypsailmgvawqqlglwlihefahhqlfknyryndlasy 190
Qy 188 FPGNPLQGFSDRWKDKHNTTHAATNVIDHGDIDLAPLFAFIPGDLCKYKASFEKAILK 247
Db 191 fvgnflqgfsqgqkqhnhvhaatcnvgrgdldlvpfyatvaehlnny--sqdswmwt 248
Qy 248 IVPYQHLTYFTAMPRLRFSTQSQVOWFKEKQMEYKYQYRNFAFEQATIVGHNAWVFYQ 307
Db 249 ifrwqhvhwtfmlpflrlswllqslfvsqmpthydyryntaiyegvgislhwawslgq 308
Qy 308 LFLPTPLRVAYFIISQMGGLLIHAHVVTNNHNSVDKYPANSRILNFPALQILITTRNM 367
Db 309 lyflpdwstrimffilshvlgvflshvvtfnhsyvekfalsnmsnyacqlqimtttrnm 368
Qy 368 TSPSPIDWLWGLNYQIEHHLPPTMPCRNACVYKVEKCKENNLPLYLVDYDFDGYAMN 427
Db 369 tpgrfidwlg9lnyqiehhlfptmtrhnlntvmlpvkfeaaanglpyvmvddyftgfwie 428
Qy 428 LQOLKNAEHIQAK 441
Db 429 lqefrnia-nvaak 441

RESULT 5

AA51355
ID AAY51355 standard; Protein; 454 AA.

XX AC AAY51355;

XX 27-APR-2000 (first entry)

DE Protein 25bce with delta6 fatty acid desaturase activity.

KW Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid;
KW transgenic plant; crop plant; delta-8-unsaturated long-chain base;
KW tolerance; resistance; soil salinity; ion stress; toxicity; drought;
KW cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
KW pharmaceutical; food; chemical raw material.

OS Unidentified.

PN DE19828850-A1.

XX 30-DEC-1999.

XX 27-JUN-1998; 98DE-1028850.

PR 27-JUN-1998; 98DE-1028850.

XX

PA (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.

PI Heinz E, Zaehringer U, Schmidt H, Sperling P;

XX WPI; 2000-127549/12.

PT New sphingolipid desaturase that selectively introduces double bond

PT into sphingolipids and capnoids -

XX Disclosure; Fig 16; 62pp; German.

XX This invention describes a novel sphingolipid desaturase that selectively
CC introduces a double bond into the sphingobase of the ceramide residue of
CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
CC desaturase, or a vector containing the DNA sequence, can be used to
CC produce transgenic plants, especially crop plants, with an increased or
CC decreased delta-8-unsaturated long-chain base content or an altered
CC delta-8-unsaturated long-chain base cis/trans ratio, especially to
CC compensate for a delta-8-unsaturated long-chain base deficiency, to
CC exclude production of delta-8-unsaturated bases, to increase tolerance
CC or resistance to soil salinity, ion stress or toxicity, drought, wet
CC conditions, cold or frost and/or phytopathogenic microorganisms, or to
CC alter size growth and flowering time. Cells, transgenic organisms or
CC plants containing the DNA sequence can be used to produce sphingolipids
CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw
CC materials. This sequence represents a protein which has delta6 fatty acid
CC desaturase activity which is described in the method of the invention.

XX Sequence 454 AA;

Query Match 44.8%; Score 1079; DB 21; Length 454;
Best Local Similarity 45.6%; Pred. No. 7e-98;
Matches 201; Conservative 84; Mismatches 140; Indels 16; Gaps 5;

Qy 12 MKVDCGKWLVLSEELVKKPGGAVIEQYRNSDATHIFAFHEGSSQAYKQLDLLKKHGEHD 71

Db 13 ikidgkwcqiddavlrshpggsaittykmdattvfhfhtgskayqwltekkceptq 72

Qy 72 E----FLEKQLEKRLDKVDINVSAYDVSVAQEKKMVESFEKLRQKLDHDDGLMKANETVFL 127

Db 73 epeipdkddpikgid--dvnmgtfnisekrsaqinksfldlrnvraegldmgsplfyi 130

Qy 128 FKAISTLSIMAFYQLVGLWYITTSACLLALAWQFGWLTHFCHQOPTKRNPLNDTISL 187

Db 131 rkiletifilfaylqlyhtyypsailmgvawqqlglwlihefahhqlfknyryndlasy 190

Qy 188 FPGNPLQ-----GFSRDWKKDKHNTTHAATNVIDHGDIDLAPLFAFIPGDLCKYKAS 240

Db 191 fvgnflqgfsqgqkqhnhvhaatcnvgrgdldlvpfyatvaehlnny--s 248

Qy 241 FEKAILKIVPYQHLTYFTAMPRLRFSTQSQVOWFKEKQMEYKYQYRNFAFEQATIVGH 300

Db 249 qdswmwtlfrwqhvhwtfmlpflrlswllqslfvsqmpthydyryntaiyegvgislh 308

Qy 301 WAWVFYQLFLPTPLRVAYFIISQMGGLLIHAHVVTNNHNSVDKYPANSRILNFPALQ 360

Db 309 wawslgqlfildwstrimffilshvlgvflshvvtfnhsyvekfalsnmsnyacqlq 368

Qy 361 ILTTRNTPSPFIDWLWGLNYQIEHHLPPTMPCRNACVYKVEKCKENNLPLYLVDY 420

Db 369 imtttrnmrpg-fidwlgwlnyqiehhlfptmtrhnlntvmlpvkfeaaanglpyvmvddy 428

Qy 421 FDGYAMNLOQLKNAEHIQAK 441

Db 429 ftgtfweieqfirnia-nvaak 448

RESULT 6

AA96722

ID AAY96722 standard; Protein; 422 AA.

CC nutrition (e.g. infant foods), animal feeds, pharmaceuticals and
CC cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes,
CC can be used to suppress expression of (II), resulting in oils with
CC increased content of saturated fatty acids.

Sequence 520 AA:

Query Match	24.68;	Score 592;	DB 22;	Length 520;	
Best Local Similarity	32.28;	Pred. No. 1.2e-49;			
Matches 146;	Conservative	79;	Mismatches 154;	Indels 74;	Gaps 15;
Qy	18	WLYLSEEL-----VKKHGGAVTEQYRNSDATIHAFHEGSSQAVKQLDLLKKHGEHD	71		
Db	115	liiikekydvstfaeqhpggtvintyfgdatgvstfh--astwskilq-----	163		
Qy	72	EFLEKQLEKRLKVDINVSAYDSVAQEK-----KMWSEFEKLQRKLHDDGLMKANETVFLF	128		
Db	164	-----nfyignlvreeptlellkeyrelraulfleqlfksksyyflf	205		
Qy	129	KAISTLSIMA-----FAPYLOYLGYWTISACLLALAWQOQFWLTHFECHQOQTKNRPLND	183		
Db	206	ktlinvsvatsiaisiyskyra--villsaslmglfqqcgwlshdfllhgvfetrwln	264		
Qy	184	TISLFFGNFLQGFSDRWKDKHNTHHAATNVIDH-----DGDIDLAPLFAPIGDCLKYK	238		
Db	265	vvgyvvgnvglfsvswwkthnlhaapnecdkytpideditlpliaawskdlatlave	324		
Qy	239	ASPEKAILKIVPYOHLXYFTAMLPMLRFSWTQSQSVQWVFK--ENOMEYKVVQORNAFWEQATI	297		
Db	325	s---ktmrlrvlqyqhlflvliltfaraswifwsaaftlrpeltigekiller-----gtm	375		
Qy	298	VGHAW-----VFYQLFLPPTWPLRVAYFIISQMGGLLIAHVVTFNHNSVDKYPANSRIL	353		
Db	376	alhyiwnsfavy---ilpgwk-pvwmvmselmsgflgyvfvlsnmgmevynts-----	427		
Qy	354	NNFAALOILTRNNTPSPFDLWGLGNLYOTEHHLFPTMPRCNLNACVKYVYKWECKENNL	413		
Db	428	kdfvnaiaasrldkagvndwfcvglnrqlehlflptmtrphnlnkispvhetlckkhgl	487		
Qy	414	PYLVDDYDFDGYAMNLOQLKNNAE---HIQAKAA	443		
Db	488	vvedvmsagcyrvlktlkdvdadaashqqlaas	520		

RESULT 8
AAY51354
ID AAY51354 standard; Protein; 525 AA.

DT 27-APR-2000 (first entry)

XX
DE protein b5pp with delta6 fatty acid desaturase activity.

KW Sphingolipid desaturase; sld; sphingobase; ceramide; capnoid;
 KW transgenic plant; crop plant; delta-8-unsaturated long-chain base;
 KW tolerance; resistance; soil salinity; ion stress; toxicity; drought;
 KW cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
 KW pharmaceutical; food; chemical raw material.

Unidentified.

XX
PN DE19828850-A1.

XX
PD 30-DEC-1999.

XX
PF 27-JUN-1998; 98DE-1028850.

XX
PR 27-JUN-1998; 98DE-1028850.

XX
XX PA (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.

PI Heinz E, Zaehrer U, Schmidt H, Sperling P;
XX
DR WPI; 2000-127549/12.

AA
PT
PT
PT

AA
PS Disclosure; Fig 16; 62pp; German.

This invention describes a novel sphingolipid desaturase that selectively introduces a double bond into the sphingobase of the ceramide residue of sphingolipids and capnoids. A DNA sequence encoding the sphingolipid desaturase, or a vector containing the DNA sequence, can be used to produce transgenic plants, especially crop plants, with an increased or decreased delta-8-unsaturated long-chain base content or an altered delta-8-unsaturated long-chain base cis/trans ratio, especially to compensate for a delta-8-unsaturated long-chain base deficiency, to exclude production of delta-8-unsaturated bases, to increase tolerance or resistance to soil salinity, ion stress or toxicity, drought, wet conditions, cold or frost and/or phytopathogenic microorganisms, or to alter size growth and flowering time. Cells, transgenic organisms or plants containing the DNA sequence can be used to produce sphingolipids and capnoids with unsaturated sphingobases. The sphingolipids or capnoids can be used in cosmetics, pharmaceuticals and foods and as chemical raw materials. This sequence represents a protein which has delta6 fatty acid desaturase activity which is described in the method of their invention.

XX	Sequence	525 AA;
SQ		

Query Match	24.5%	Score 590.5;	DB 21;	Length 525;
Best Local Similarity	32.5%;	Pred. No. 1.7e-49;		
Matches 140;	Conservative	76;	Mismatches 160;	Indels 55;
				Gaps 12;

RESULT

RESULTS 9
AAB46810
ID AAB46810 standard; Protein; 525 AA.

XX AAB46810;

Db 249 ltrmwsrf-----mvlngtqwfypilslfarslswclqsilflvlpngqahkpsgarvpisl 302
QY 292 WEQATIVGHAWVYQLELLPTWPLR-VAYFTIISQMGGLLIAHVTFNHNHNSVDKYPANS 350
Db 303 veqlslamhwtwylatmflfikdpvnmlyflvsqavcgnllaivfslnhngmpviskee 362
QY 351 RILNFAALQILTRNMTSPFPIDMLWGLNYQIEHHLFPTMPRCNLNACVKYKEMCKE 410
Db 363 avdmdftkqitgrdvhpglfanwftgglngyqiehhlfpsmprhnfskiqpavetlckk 422
QY 411 NNLPYLVDYDFGYAMNLOQLKNAE 436
Db 423 ynvryhtgmiegtaevfslnevs 448

RESULT 15

AAV56045
ID AAV56045 standard; Protein; 457 AA.

XX AC AAV56045;

XX DT 28-MAR-2000 (first entry)

XX DE Fungal delta6-desaturase protein sequence.

XX KW Polyunsaturated fatty acid; fungus; delta6-desaturase; animal feed;
XX KW transgenic animal; malnutrition; biosynthesis.

XX OS Unidentified.

XX PN WO9961602-A1.

XX PD 02-DEC-1999.

XX PF 28-MAY-1999; 99WO-US12088.

XX PR 29-MAY-1998; 98US-0087578.

XX PA (OHIS) UNIV OHIO STATE.

XX PI Kopchick JJ, Kelder B, Huang Y, Kirchner SJ, Mukerji P;

XX DR WPI; 2000-072619/06.

XX DR N-PSDB; AAZ47129.

XX PT Producing essential fatty acids and long-chain polyunsaturated fatty
XX PT acids, for use in nutritional, animal feed and medical formulations -

XX PS Disclosure; Fig 9; 71pp; English.

XX CC The invention relates to a method of generating novel compositions
XX CC comprising animal cells producing essential fatty acids (FAs). The animal
XX CC cells are produced by transforming cells, e.g. embryonic stem cells, with
XX CC nucleic acid encoding heterologous enzymes involved in fatty acid,
XX CC e.g. long chain or polyunsaturated fatty acid (PFA) biosynthesis. This
XX CC sequence corresponds to a fungal delta6-desaturase whose coding sequence
XX CC is an example of a nucleic acid sequence used to transform the cells. The
XX CC essential FAs obtained can be used in nutritional formulations or animal
XX CC feed formulations. The long chain PFAs can be used in nutritional
XX CC formulations, cosmetic formulations or animal feed formulations. The
XX CC products can also be used for producing transgenic animals which can be
XX CC used for producing essential FAs which can be used for producing
XX CC downstream products such as leukotrienes, thromboxanes, arachidonic acid,
XX CC eicosapentaenoic acid or docosahexaenoic acid. The products can also be
XX CC used in cell culture. The animal or milk fat produced can be administered
XX CC to treat malnutrition.

XX SQ Sequence 457 AA;

Query Match 23.1%; Score 557; DB 21; Length 457;
Best Local Similarity 32.1%; Pred. No. 2.9e-46;
Matches 143; Conservative 64; Mismatches 187; Indels 52; Gaps 11;

QY 12 MKVDGKWLVLSELYKHPGGAVIEQYRNSDATHIFHAFHEGSSQAYKQLDLLKKHGEHD 71
Db 34 miidnk-vydvrefpdpbgssviltvhgkqgtdvdfthpeaaw----- 77
QY 72 EFLEKOLEKRLDKVDINVSAYDVSVAQEKMMVESFEKLRQKLHDDGLMKANETYFLFKAI 131
Db 78 etlanfyvgdidesdrdiknddfa-aevrklrtlfqsl-----gydsskayafkvs 129
QY 132 STLSTMAFAFYLOYLGW-----YITSACLALAAWQOFGWLTHERFCHQOPTKNSPLNDT 184
Db 130 fnlcwglstvi-vakwgtstlanvlsaallglfwqcgwiahdfllhqvfqdrfwgdl 188
QY 185 ISLFFGNFLQGFSDWWDKDKHNTTHAATNVIDHDGIDIDLAPL-----FAFIPG-D 233
Db 189 fgafllggvcqgfsfsswwkdkhthhaapnvghedpdidthplltwsehalenfsdvpee 248
QY 234 LCKYKASFEKAILKIVPYOHLFTAMLPMRLFSWTGQSVQWVFKENQMEYKYVQR--NAF 291
Db 249 ltrmwsrf-----mvlngtqwfypilslfarslswclqsilflvlpngqahkpsgarvpisl 302
QY 292 WEQATIVGHAWVYQLELLPTWPLR-VAYFTIISQMGGLLIAHVTFNHNHNSVDKYPANS 350
Db 303 veqlslamhwtwylatmflfikdpvnmlyflvsqavcgnllaivfslnhngmpviskee 362
QY 351 RILNFAALQILTRNMTSPFPIDMLWGLNYQIEHHLFPTMPRCNLNACVKYKEMCKE 410
Db 363 avdmdftkqitgrdvhpglfanwftgglngyqiehhlfpsmprhnfskiqpavetlckk 422
QY 411 NNLPYLVDYDFGYAMNLOQLKNAE 436
Db 423 ynvryhtgmiegtaevfslnevs 448

Search completed: August 6, 2002, 16:21:54

Job time: 1063 sec

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OM protein - protein search, using sw model

Run on: August 6, 2002, 16:16:26 ; Search time 15.83 Seconds
(without alignments)
683.546 Million cell updates/sec

Title: US-09-555-093-2

Perfect score: 2410

Sequence: 1 MYVDKNASGLRMKVDGKWL.....YAMNLOQLKNMAEHIOAKAA 443

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	557	23.1	457	2	US-08-834-655-2
2	557	23.1	457	3	US-08-834-033A-2
3	557	23.1	457	4	US-09-363-574-2
4	555	23.0	457	2	US-08-833-610-4
5	555	23.0	457	3	US-08-834-033A-14
6	501	20.8	355	2	US-08-834-655-5
7	501	20.8	355	3	US-08-834-033A-6
8	501	20.8	355	4	US-09-363-574-5
9	456.5	18.9	446	2	US-08-833-610-5
10	456.5	18.9	446	3	US-08-834-033A-15
11	448.5	18.6	448	1	US-08-366-779-5
12	448.5	18.6	448	1	US-08-789-936-5
13	448.5	18.6	448	4	US-08-934-254-5
14	412	17.1	87	2	US-08-834-655-10
15	412	17.1	87	3	US-08-834-033A-11
16	412	17.1	87	4	US-09-363-574-10
17	400	16.6	452	4	US-08-934-254-27
18	259.5	10.8	252	2	US-08-834-655-7
19	259.5	10.8	252	3	US-08-834-033A-8
20	259.5	10.8	252	4	US-09-363-574-7
21	217	9.0	365	2	US-08-833-610-7
22	217	9.0	365	3	US-08-834-033A-17
23	215.5	8.9	359	1	US-08-307-382-2
24	215.5	8.9	359	1	US-08-366-779-2
25	215.5	8.9	359	1	US-08-478-727-2
26	215.5	8.9	359	1	US-08-473-508-2
27	215.5	8.9	359	1	US-08-789-936-2

28 215.5 8.9 359 2 US-08-833-610-6
29 215.5 8.9 359 3 US-08-834-033A-16
30 215.5 8.9 359 4 US-08-934-254-2
31 186 7.7 446 2 US-08-833-610-2
32 186 7.7 446 3 US-08-834-033A-5
33 174.5 7.2 443 4 US-09-161-994A-3
34 166 6.9 143 2 US-08-834-655-11
35 166 6.9 143 3 US-08-834-033A-12
36 166 6.9 143 4 US-09-363-574-11
37 164.5 6.8 418 5 PCT-US94-01321-72
38 161 6.7 131 2 US-08-834-655-9
39 161 6.7 131 3 US-08-834-033A-10
40 161 6.7 131 4 US-09-363-574-9
41 149 6.2 125 2 US-08-834-655-8
42 149 6.2 125 3 US-08-834-033A-9
43 149 6.2 125 4 US-09-363-574-8
44 148 6.1 424 4 US-09-161-994A-4
45 141.5 5.9 384 4 US-09-354-231B-18

ALIGNMENTS

RESULT 1

US-08-834-655-2
; Sequence 2, Application US/08834655
; Patent No. 5968809
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MURKERJL, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,655
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RAE-VENTER, BARBARA
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.124.000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 328-4400
; TELEFAX: (650) 328-4477
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-834-655-2

Query Match 23.1%; Score 557; DB 2; Length 457;
Best Local Similarity 32.1%; Pred. No. 7.6e-47;
Matches 143; Conservative 64; Mismatches 187; Indels 52; Gaps 11;

[illegible]

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RESULT      2
US-08-834-033A-2
; Sequence 2, Application US/08834033A
; Patent No. 6075183
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MUKERJII, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH AND LIMBACH, L. L. P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,033A
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-300, USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-834-033A-2

Query Match          23.1%; Score 557; DB 3; Length 457;
Best Local Similarity 32.1%; Pred. No. 7.6e-47;
Matches 143; Conservative 64; Mismatches 187; Indels 52; Gaps 11

Qy 12 MKVDGKWLILSEELVKKHPGCAVLEQYRNSDATHIFAHFHEGSSQAYQLDLLKKHGEHD 71
Db 34 MILDNC-YVDVREFPDHPGGSVILTHVGKGOGTDVDFTHPEAAW-----77
Qy 72 EFLEKQLEKRLDKVDINVSAYDVSAQEKMKVESFEKLRQKLHDDGLMKANETYFLFKAI 131
Db 78 ETLANFYVGDI DESDRDIKNDEFA-AEVRKLRTLFQSL-----GYDSSKAYAFKVS 129
Qy 132 STL SIMAFAYLQYLGW-----YITISACILALAWQOGFWLTHFEFCHQOPTKRNPLNDT 184
Db 130 FNLICIGWLSYVI-VAKWGQSTLANVLVSAALLGLFWQCGWLAHDFLHHQVQDFRWGDL 188
Qy 185 ISLFFGFLQCFGRDWNKDKHTHAANVNIHDHGDIDLAPL-----FATIPG-D 233
Db 189 FGAFLGGVCQGFSSWKKDKINTHAAPNVHGEDPDIDTHPLLTWSEHALENFSDVPDEE 248
Qy 234 LCKYKASFEKAILKIVPYQHLYFTAMLPMLRFSWTGQSVQVFKENQMEYKVVQR--NAF 291
Db 249 LTRMWSRF-----MVLNQTFWFYFPIILSFARLSWCLQSLFVLVPGCAHKKPSGARVPISL 302
Qy 292 WEQATIVGHWAWEYQLFLPTWPLR-VAYFTIISOMGGLLIAHVVTFTNHSVDKYPPANS 350
Db 303 VEQLSLAHHTWYLATWELFKDPVNMILVYFLVSAQVCNLLAIVFSLNHNGMPVISKEE 362
Qy 351 RILNFAALQILTRNMTSPFIDWLMGLNQYIEHHLFPTMPRONLACVYKVECKE 410
Db 363 AVDMDFETKIIITGRDVHPGLFANWFTGGLNYQIEHHLFSPMRHNSFKIQPAVETLCKK 422
Qy 411 NNLPLYLVDYDYGAMNLQQLKNAE 436
Db 423 YNVRHYTGMIEGTAEVFSRLNEVSK 448

RESULT 3
US-09-363-574-2
; Sequence 2, Application US/09363574
; Patent No. 6136574
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/363,574
; FILING DATE:

```

```

: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: WARD, MICHAEL R.
: REGISTRATION NUMBER: 38,651
: REFERENCE/DOCKET NUMBER: CGAB-202 USA
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 433-4150
: TELEFAX: (415) 433-8716
: TELEX: N/A
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 457 amino acids
: TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-09-367-574-2

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[illegible]

```

RESULT      4
US-08-833-610-4
; Sequence 4, Application US/08833610
; Patent No. 5972664
; GENERAL INFORMATION:
; APPLICANT: KUTUZZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND
; TITLE OF INVENTION: OF LONG CHA
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSES: RAB-VENTER LAW GROUP
; STREET: 260 SHERIDAN AVE, P.O.
; CITY: PALO ALTO

```

```

; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,610
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RAE-VENTER, BARBARA
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.123.00US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)328-4400
; TELEFAX: (650)328-4477
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-833-610-4

Query Match      23.0%; Score 555; DB 2; Length 457;
Best Local Similarity 32.1%; Pred. No. 1.2e-46;
Matches 143; Conservative 64; Mismatches 187; Indels 52; Gaps 11;

QY 12 MKVDGKWLYLEELVKKHGGAVIEQVNSDATHIFHAFHEGSSQAQKQLDLLKKHGHD 71
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 34 MIIDNK-VYDVREVPDPHGGSVTLTHVGKDGTDFDTTFPEAAW----- 77

QY 72 EFLEKLEKRDKYDINVSAVDVSVAOEKKVSEFKLRQKLHDDGLMKANETYFLFKAI 131
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 78 ETLANFYVGDI DESDRDIKNDDFA-AEVRKLTILFQSL-----GYDSSKAIFYAFKVS 129

QY 132 STLSTIMAFAYLYLGM-----YITSACLLALAWOQFGWLTHEFCHQOPTKNRP LNDT 184
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 130 FNLCITWGLSTVI-VAKMGQTSTLANVLISAALLGLFWQCQGWLAHDFLHHQVFQDRFWGDL 188

QY 185 ISLPFGNFLOGFSRDWKDKINTHTHAATNTVIDHGDIDLAPL-----FAFIG-D 233
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 189 FGALFVGVCQGFSRWKDKINTHTHAAPNVHVEDPDIDTPLLTWSEHALEMFS DVPDEE 248

QY 234 LCKYKASFEKAILXIVPYQHLYFTAMPLMFRSFTGSQVOWFKENOMEXKYVQR--NAF 291
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 249 LTRWSRF-----MVLNWTWFYPILLSFARLSNCLQSILFVLPNGQAHRFSGARVPISL 302

QY 292 WEQATIVGHWAWPYQQLFLTPTWPLR-VAFPIISQMGGGLLIAHVVTFNHNSVDKYPANS 350
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 303 VEQUSLAHMHWYLATMFLFTKDPVNMLVYFLVSQA VCGNLALTIVFSLNHNGMPVISKEE 362

QY 351 RILNFAALQILTTRNTPTSPFDIWLGGGLNYQTEHLHFTPMPCNCINACVKYVKWECKE 410
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 363 AVDMDFETKLIITGRDVHPGLFANWFFTGGLNQIEHLHFPSMPRNHSKI QPAVETLCKK 422

QY 411 NNLPYLVDVDPDG YAMNNLQQLKNMAE 436
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 423 YNVRTYTGMTIEGTAEVFSRLNEYSK 448

RESULT 5
US-08-834-033A-14
; Sequence 14, Application US/08834033A
; Patent No. 6075183
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
```

RESULT 5
US-08-834-033A-14
; Sequence 14, Application US/08834033A
; Patent No. 6075183
; GENERAL INFORMATION:
; APPLICANT: KNIITZON, DEBORAH

APPLICANT: MUKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESSES:
ADDRESS: LIMBACH AND LIMBACH, L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
FILING DATE: 11-APR-1997
APPLICATION NUMBER: US/08/834,033A
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-300.USA
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-033A-14

Query Match 23.0%; Score 555; DB 3; Length 457;
Best Local Similarity 32.1%; Pred. No. 1.2e-46;
Matches 143; Conservative 64; Mismatches 187; Indels 52; Gaps 11;

QY 12 MKVDGKWLILSEELVKKHGGAVTEQYRNSDATHIEHAFHEGSSQAYKQLDLLKKHGEHD 71
Db 34 MIIDNK-VYDVFVDPHGGSVILTHVGKDGTDVDTFPEAAW----- 77
QY 72 EFLEKQLEKRLDKYDINVSAYDVSVAQEKMKVESFEKLRQLKHDGGLMKANETYFLFKRAI 131
Db 78 ETLANFYVGDIDESDRDIKNDDFA-AEVRKLTFLQSL-----GYDSSKAYIAFKVS 129
QY 132 STLIMAFAYLQYLGW-----YITSACLLALAWQFGLWTFEFCQQPTKNRPLNDT 184
Db 130 FNLICWGLSTVI-VAKWGQSTLANVLNSAALLGLFWQCGWLAHDFLHHQVDFRFGDL 188
QY 185 ISLFFGNFLOGFSRDWKKDKHNTHAATNVIDHGDIDLAPL-----FAFIG-D 233
Db 189 FGAFLGGVCGQFSSWKKDKHNTHAAPNHHVEDPDIDTPLLTSWSEHALEMFSVDPDEE 248
QY 234 LCKYKASFKAALKIVPYQHLYFTAMPLMPLRFSWTGOSVQWVFKENQMEYKVYQ--NAF 291
Db 249 LTRWSRF-----MVLNQTWFYFPILSFARLSWCLQSILFVLPNGQAHKPSGARVPISL 302
QY 292 WEQATIVGHNAWVYQLFLLPTWPLR-VAYFIISOMGGLLIAHVTFNHNVDKYPANS 350
Db 303 VEQLSLAMHWTWYLATMFLFKIDPVMNLVFLVSOAVCGNLLAIVFLSNHNGMPVISKEE 362
QY 351 RILANFAALQILTRNTPSPFIDMLGGLNLYQTEHLFPTMPRCNLNACVKYKWECKE 410
Db 363 AVDMDFTKIITORDVHPGLFANWFTGGLNYQIEHLFLFSPMPRHNFSKIQPAVETLCKK 422

QY 411 NNLPYLVDDYFDGYAMNQLQKNMAE 436
Db 423 YNVRYHTTGMTEGTAEVESRLNEYSK 448

RESULT 6

US-08-834-655-5
Sequence 5, Application US/08834655
Patent No. 5968809
GENERAL INFORMATION:
APPLICANT: KNUZON, DEBORAH
APPLICANT: MUKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESSES:
ADDRESS: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,655
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.124.000S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
TELEFAX: (650) 328-4477
TELEX: N/A
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-655-5

Query Match 20.8%; Score 501; DB 2; Length 355;
Best Local Similarity 34.3%; Pred. No. 1.8e-41;
Matches 120; Conservative 48; Mismatches 154; Indels 28; Gaps 7;

QY 108 KLKQLKDDGLMKANETYFLFKALSTLSIMAFAYLQYLGW-----YITSACLLALAW 160
Db 4 KLRTLFQSLGYDSSKAYIAFKVSFNLICWGLSTVI-VAKWGQSTLANVLNSAALLGLFW 62
QY 161 QQCGWLTFEFCQQPTKNRPLNDTISLFFGNFLOGFSRDWKKDKHNTHAATNVIDHGD 220
Db 63 QCCGWLADHDFLHHQVDFRFGDLFGAFLGGVCGQFSSWKKDKHNTHAAPNVHGEDPD 122
QY 221 IDLAPL-----FAFIG-DLCKYKASFKAALKIVPYQHLYFTAMPLMPLRFSWTG 269
Db 123 IDTHPLLTWSSEHALEMFSVDPDEELTRWSRF-----MVLNQTWFYFPILSFARLSWCL 176
QY 270 QSVQWVFKENQMEYKVYQ--NAFWEQATIVGHNAWVYQLFLLPTWPLR-VAYFIISOM 326
Db 177 QSILFVLPNGQAHKPSGARVPISLVEQLSLAMHWTWYLATMFLFKIDPVMNLVFLYSQA 236
QY 327 GGGLLIAHVVTNHNVDKYPANSRI LNFAALQILTRNTPSPFIDMLGGLNLYQIEH 386

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Db 177 QSILEVLPNGQAHKPSGARVPISLVEQSLAMHWTWYLATMFLFKDPVNMVLVFLVSQA 236
Qy 327 GGLLIAHVVTFNHNSVDKYPANSRILNNFAALQILTRNMTSPSPFDLWGLGNTQIEH 386
Db 237 VCGNLLAIVFSLHNHMPVISKEEAVDMDFFTKQIITGRDVHGLFANFTGGLNTQIEH 296
Qy 387 HLFPTMPCNLNACVYKWKCKENNLPLYVDDYDFGYYAMNLOQLKNMAE 436
Db 297 HLFPSMPRHNSFKIOPAVETLCKKYNVRYHTTGMIETGAEVFSRLNEVSK 346

RESULT 8
US-09-363-574-5
; Sequence 5, Application US/09363574
; Patent No. 6136574
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MORKERJL, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESS: LIMBACH AND LIMBACH L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/363.574
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-202 USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-363-574-5

Query Match 20.8%; Score 501; DB 4; Length 355;
Best Local Similarity 34.3%; Pred.No. 1.8e-41;
Matches 120; Conservative 48; Mismatches 154; Indels 28; Gaps 7

Qy 108 KLRQKLDDGLMKANETVFLFKAIKSTLSIMAFVLYQLGW-----YITSACILALAW 160
Db 4 KLRTLFQSLGYDDSSKAYAFKVSFNLCTWGLSTVI-VAKWGQTSTLANVLSAALLGLEW 62
Qy 161 QQFGWLTTFEFCQOPTKRNPLNDTISLFFGNLQGFSDRWMKDKHNTHHAATNVIDHGD 220
Db 63 QOCQGLAHDFLHHQVQDFRFGDLFGAFLGGVQCQGFSSSWKDKHNTHHAAPNVHGEDPD 122
Qy 221 IDLAPL-----FAFIPG-DLCKYKASEKALKIVPYQHLVFTAMLPLMRSWTC 269
Db 123 IDTHPLLWTSEHALEMFSDVDPDELTMRMSRF-----MVLNQTWFFYFILLSFARLSWCL 176

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; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-366-779-5

Query Match      18.6%; Score 448.5; DB 1; Length 448;
Best Local Similarity 27.9%; Pred No 4e-36;
Matches 127; Conservative 71; Mismatches 186; Indels 71; Gaps 15;

QY 10 LRMKVDGKWLYLSEELYKKHPGGAV-IEQYRNSDATHIFAHFEGSSQAYKQLDLLKKHG 68
   | : | | : | | | | : | | | | : | | | | :
Db 23 LWSIQCK-AYDSDWKVDHPGGSFPLKSLAGQEVTDAFVAFHPASTW----- 69

QY 69 EHDEFLEKQLEKRLDKVDINVSAYDSVAQ-----EKKMVSEFEKLRKQLHDDGLMKANET 124
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 70 -----KNLDKFFTYGLKDYSEVSESKDYRKLVPFEFSKM--GLYD-----KKG 110

QY 125 YELFKAISTLSIMAFAYLVQYLG-----WYITSACLALAAQOFGWLTFECHOQPT 176
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 111 HIRP---ATLCFTAMLFAMSVGYLVFCGEVLVHLFGCLMGFLWISQWIGHDAGHYWV 167

QY 177 KNPLNDTISLFFGNFLQGFSDRWKDKHNTHTHAATNVIDHDGIDIDLAP-----LFAF 229
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 168 SDSRLANKFMGIFRANCLSGISIGWKNNHNAHIAACSLEYDPLQIYIPFLVSSKFFGS 227

QY 230 IPGDLCKYKASFKAIIUKIYVQHLTYTAMLPMLRFSWTGOSVQWVKENQMEYKVVQRN 289
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 228 LTSHFYEKRLTFDSLSRFFVSQHWTFYPIPMCAARLNMYVQSLLMLLTKRNVSYRAQE-- 285

QY 290 AFEQATIVGHAW-VFYQLFL--LPMPRLRVAYFIIISQMGGLLIAHVVTFNHNSVDKY 346
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 286 -----LLGCLVFSIWYPLLVSCLPNWGERIMEVIAASLSVTGMQOQVO-FSLNHFFSSVY 337

QY 347 PANSRILNFAALQILTRNNTPSPFIDWLWGLNLYQIEHHLFTPMPCNLNACVKYVKE 406
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 338 VGKPK-GNNVFEKQTDGTLDISCPWMDWFGHGSQFQIEHHLFPKMPRCNLKISPYVIE 396

QY 407 WKENNLPLYVDVDFDGYANMLOQLKNMAEHIQAK 441
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 397 LCKKHNLPLYNYSFSAKANEMTLRLNTA--LQAR 429

RESULT 12
US-08-789-936-5
; Sequence 5, Application US/08789936
; Patent No. 5789220
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; APPLICANT: Reddy, Avutu S.
; APPLICANT: Nuccio, Michael
; APPLICANT: Freyssinet, Georges L.
; APPLICANT: Nunberg, Andrew N.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; TITLE OF INVENTION: DELTA 6-DESATURASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/789, 936

```


APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,655
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.124.000US
TELEPHONE: (650) 328-4400
TELEFAX: (650) 328-4477
TELEX: N/A
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-655-10

Query Match 17.1%; Score 412; DB 2; Length 87;
Best Local Similarity 90.0%; Pred. No. 1.5e-33;
Matches 72; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
Qy 364 TRNMTSPFIDWLWGLNYQIEHHLFTMPRCNLNACVYKWKCKENNLPLYLVDYDFG 423
Db 8 TRNMTSPFIDWLWGLNYQIEHHLFTMPRCNLNRCMKYKWKCAENNLPLYLVDYDFG 67
Qy 424 YAMNLOQLKNAEHIOAKA 443
Db 68 YNLNLOQLKNAELVQAKA 87

RESULT 15
US-08-834-033A-11
Sequence 11, Application US/08834033A
Patent No. 6075183
GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MUKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,033A
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-300.USA
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-033A-11
Query Match 17.1%; Score 412; DB 3; Length 87;
Best Local Similarity 90.0%; Pred. No. 1.5e-33;
Matches 72; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
Qy 364 TRNMTSPFIDWLWGLNYQIEHHLFTMPRCNLNACVYKWKCKENNLPLYLVDYDFG 423
Db 8 TRNMTSPFIDWLWGLNYQIEHHLFTMPRCNLNRCMKYKWKCAENNLPLYLVDYDFG 67
Qy 424 YAMNLOQLKNAEHIOAKA 443
Db 68 YNLNLOQLKNAELVQAKA 87
Search completed: August 6, 2002, 16:22:16
Job time: 350 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 01:36:14 ; Search time 81.96 Seconds
(without alignments)
4381.603 Million cell updates/sec

Title: US-09-555-093-1

Perfect score: 1462
Sequence: 1 gtcacacaaatgtctcg.....aataaaccttgttttcaa 1462

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_NA.*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	6.6	1617	2	US-08-834-655-1
2	97	6.6	1617	3	US-08-834-033A-1
3	97	6.6	1617	3	US-09-363-574-1
4	68.4	4.7	1684	2	US-08-831-570-1
5	68.4	4.7	1684	2	US-08-831-575-1
6	68.4	4.7	1685	1	US-08-366-779-4
7	68.4	4.7	1685	1	US-08-789-936-4
8	68.4	4.7	1685	4	US-08-934-254-4
9	41.6	2.8	1702	4	US-08-934-254-26
10	41	2.8	7218	1	US-08-232-463-14
11	39.8	2.7	3369	2	US-08-619-198-2
12	39.8	2.7	4170	2	US-08-619-198-2
13	39.8	2.7	5192	2	US-08-619-198-8
14	39.8	2.7	5198	2	US-08-619-198-1
15	39	2.7	2277	1	US-08-676-567-2
16	39	2.7	2277	1	US-08-676-974-2
17	39	2.7	2277	2	US-09-098-487-2
18	37.8	2.6	1129	4	US-09-227-357-40
19	37.6	2.6	144	1	US-08-702-344-26
20	37.2	2.5	19124	2	US-08-487-826B-13
21	36.8	2.5	2223	1	US-08-257-073-4
22	36.4	2.5	719	3	US-08-714-918-11
23	36.4	2.5	719	4	US-09-265-315-11
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25	36.4	2.5	719	4	US-09-266-417-11
26	36.4	2.5	1098	3	US-09-248-335-35
27	35.8	2.4	1474	4	US-08-821-994-04

28 35.8 2.4 56516 2 US-08-996-306-1 Sequence 1, Appli
29 35.8 2.4 56516 4 US-09-338-907-1 Sequence 1, Appli
30 35.8 2.4 56516 4 US-09-218-207-1 Sequence 1, Appli
31 35.8 2.4 56520 4 US-09-338-907-179 Sequence 179, App
32 35.8 2.4 56520 4 US-09-218-207-179 Sequence 179, App
33 35.2 2.4 991 4 US-08-793-634B-3 Sequence 3, Appli
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35 35.2 2.4 7218 1 US-08-232-463-14 Sequence 14, Appli
36 35 2.4 2628 3 US-08-143-219-1 Sequence 1, Appli
37 35 2.4 2852 3 US-09-027-137-2 Sequence 2, Appli
38 35 2.4 246240 2 US-08-724-394A-20 Sequence 20, Appli
39 35 2.4 246240 2 US-08-724-394A-21 Sequence 21, Appli
40 35 2.4 246240 2 US-08-724-394A-22 Sequence 22, Appli
41 34.8 2.4 1428 2 US-08-786-999-2 Sequence 2, Appli
42 34.8 2.4 1428 4 US-08-969-987-8 Sequence 8, Appli
43 34.8 2.4 1491 4 US-08-999-774A-7 Sequence 7, Appli
44 34.8 2.4 1494 1 US-08-585-758A-3 Sequence 3, Appli
45 34.8 2.4 1494 1 US-08-977-818-3 Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-834-655-1
; Sequence 1, Application US/08834655
; Patent No. 5968809
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MORKERJL, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESS: RAE-VENTER LAW GROUP, P.C.
; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,655
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RAE-VENTER, BARBARA
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.124.000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 328-4400
; TELEFAX: (650) 328-4477
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1617 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-834-655-1

Query Match 6.6%; Score 97; DB 2; Length 1617;
Best Local Similarity 47.2%; Pred. No. 8.1e-17;
Matches 415; Conservative 0; Mismatches 440; Indels 24; Gaps 3;

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Qy 464 tctgcatgtttattagcacttgacgcaacaattcggatgtgttaacacatgagttctgc 523
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Db 536 TCGGCTGCGCTTTTGGGCTGTCTGCGCAGCAGTGGGATGGCTCACGACTTTTGG 595
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Qy 524 catcaacagcacaacaagaacagaccttgaatgatactattcttcttcttggtta 583
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Db 836 TTCATGGTCTGAACAGACCTGTTTACTTCCCATCTCTGTTGCGCGTCTCTCC 895
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Qy 863 gtctatcaagaagaatgcttcttgggagcaagcaacaattgttggcattgggctgggta 922
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Qy 980 tcacaaatgggagggagccttttattgctcagctagtcactttcaacataaactctgtt 1039
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Db 1076 TCGCAGCGGTTGCGGAACCTTGTGGGATCGTGTTCTCGCTCAACCAACAGGTATG 1135
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Qy 1040 gataagtatccagccaattctcgaattttaacaaacttcgcgcctcttcaaatattgacc 1099
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Db 1196 GGTGATGATCCACCCGGGCTATTGCGCAACTGGTTACGGGGTGGATTGAACATATCAG 1255
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Qy 1160 atcagaccactgtttcccaacaatgcccagtttgcaatctgaaatgcttgcgtgaaat 1219
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Db 1256 ATCAGACCACTGTTCCCTTCGATGCTCGCCACAACATTTCNAAAGATCCAGCCTGCT 1315
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Qy 1220 gtgaagaatggtgcaagagaataaattcttccctacctcgtcgatgactatttgacgga 1279
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RESULT 2

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US-08-834-033A-1
; Sequence 1, Application US/08834033A
; Patent No. 6075183
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MUKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
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; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,033A
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-300.USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1617 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-834-033A-1
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Query Match 6.6%; Score 97; DB 3; Length 1617;

Best Local Similarity 47.2%; Pred. No. 8.1e-17;

Matches 415; Conservative 0; Mismatches 440; Indels 24; Gaps 3;

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Qy 464 tctgcatgtttattagcacttgacgcaacaattcggatgtgttaacacatgagttctgc 523
|| || || || || || || || || || || || || || || || || || || || ||
Db 536 TCGGCTGCGCTTTTGGGCTGTCTGCGCAGCAGTGGGATGGCTCACGACTTTTGG 595
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Db 836 TTCATGGTCTGAACAGACCTGTTTACTTCCCATCTCTGTTGCGCGTCTCTCC 895
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Qy 809 tggactggtcagtcagttcaatgggtatt-----caagagagaatcaaatggagtagaag 862
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```


APPLICANT: Nunberg, Andrew N.
APPLICANT: Beremand, Phillip D.
TITLE OF INVENTION: A SUNFLOWER ALBUMIN 5' REGULATORY REGION
TITLE OF INVENTION: FOR THE MODIFICATION OF PLANT SEED LIPID
TITLE OF INVENTION: COMPOSITION
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/831,570
FILING DATE: 09-APR-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10545
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 743-4366
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1684 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 43..1387
US-08-831-570-1

Query Match 4.7%; Score 68.4; DB 2; Length 1684;
Best Local Similarity 44.2%; Pred. No. 4.le-09;
Matches 423; Conservative 0; Mismatches 526; Indels 9; Gaps 3;

Qy 381 catattctctgttaaacgatttcaacacatttcaattatgacattgcatatttatttc 440
Db 386 CAACCTTTGTGCTTTATAGCAATGCTGTTGCTATGAGTGTATGGGGTGTGTTTGTG 445
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Db 446 AGGGTGTGTTTGGTACATTTGTTTCTTGGTGTGTTGATGGGTCTTTGGATTGAGATG 505
Qy 501 gatggttaaacacatgagttctgcatcacatcacgccaacaaagacagacctttgaatgata 560
Db 506 GTTGATTGGACATGATGCTGGCATTATATGCTAGTCTGATTCAAGGCTTAATAAGT 565
Qy 561 ctattctctgttctgttgtaattcttcaagagattttcaagattttcaagattggtggagagaca 620
Db 566 TTATGGGTATTTTGTCTGCAAAATGCTTTTCCAGGAATAAGTATTTGGTTGGTGGAAATGGA 625
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Qy 681 cacaacttttcgatttattccagagagatttgcgaagtataaagccagctttgaaaaag 740
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Qy 741 caattctcaagattgtaccatatcaacatctctattttcacgcgaatgcttc---caatgc 797
Db 746 AAAGTTGACTTTTGACTCTTTATCAAGATTCTTTGTAAGTTATCAACATGGACATTTT 805

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Db 806 ACCCTATTATGTGTGCTGCTAGGCTCAATATGTATGTACAAATCTCTCATAATGTTGTTGA 865
Qy 858 acaaggtctatacaaaagaaatgcattctctggagcaagcaacaattgttgacattgggett 917
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RESULT 5

US-08-831-575-1
; Sequence 1, Application US/08831575
; Patent No. 597436
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; APPLICANT: Li, Zhongsen
; TITLE OF INVENTION: AN OLEOSIN 5' REGULATORY REGION FOR THE
; TITLE OF INVENTION: MODIFICATION OF PLANT SEED LIPID COMPOSITION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/831,575
; FILING DATE: 09-APR-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:


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; LENGTH: 1684 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..1387
US-08-831-575-1

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Query Match	4.78;	Score 68.4;	DB 2;	Length 1684;
Best Local Similarity	44.23;	Pred. No. 4.1e-09;		
Matches 423;	Conservative 0;	Mismatches 526;	Indels 9;	Gaps 3;
QY	381	catatttcctgtttaaagcggatttcaacacactttcaattatggcatttgacatttcatcttattcttc	440	
DB	386	CAACTTGTGCTTTATACCAATGCTGTTGCTATACAGTCTTTATGGGCTTTGTTTGTG	445	
QY	441	agtatcttggatgtatattactctgcattcttagcacttgcattgcgcacaaactcgg	500	
DB	446	AGGCTGTTTGGTACATTTGTTTCTGGTGTTTATGGGCTTTGATGGGCTTTCTTTGGATTCAGATG	505	
QY	501	gatgttlaaacatgatgtctgcatacaacagcacaacaaagacagaccttggatgata	560	
DB	506	GTTGAGATGGACATGATGCTGGCATTTATATGTTAGTGTCTGATTCAGGCTTTATAAGT	565	
QY	561	ctattcttgttcttggtaattcttcacaggaatttccaagagatttccaagagatttggcgaaggaca	620	
DB	566	TTATGGGTATTTTTCGTCGCAATTTGCTCTTCAGGAATAAGTATTGGTTGGTGGAAATGGA	625	
QY	621	agcataacatcatcagctgcgcacaaatgtaattgatcatcagcggatcatcagactcgg	680	
DB	626	ACCATAATGACATACATATGCCCTGTATAGCCCTTGAATATGACCTCATTTACAATATA	685	
QY	681	caccacttttcgcatatttccacaggagatttgcgaagtataaaggccagcttttgaaaaag	740	
DB	686	TACCATTCTTGTGTCCTTCACCAAGTTTTTGGTTCACTCACTCACTCTCATTTCTATGAGA	745	
QY	741	caattctcaagattgttaaccatacaacatctctatttccagcgaatgctc---caatgc	797	
DB	746	AAAGGTTGACCTTTTGACTCTTTATCAAGATTCCTTTGAAGTTATCAACATTTGGACATTTT	805	
QY	798	tcqgttctcatgacatgggtcagtcagttcaatgggtattccaagagaaatcaaatggagt	857	
DB	806	ACCTATTATGTGCTGCTAGGCTCAATATGATGTACAAATCTCTATAATGTTGTTGA	865	
QY	858	acaaggtctatcaagaataatgcatctctgggagcgaagcaacaatttgttgacattgggctt	917	
DB	866	CCAAGAGAAATGTCTCTATCGAGCTCAGGAACCTTTGGGATGCTAGTTCGATTT	925	
QY	918	gggtattctatcaattgttcttattacacatcggcgaactcgggttgcctatttcatcta	977	
DB	926	GGTACCCGGTTGCTTTGTTCTTTGCTTAATTTGGCTTAATTTGGGTTGAAGAATAATGTTTGTATTG	985	
QY	978	ttcacaaaaggaggggaccttttgattgctcagtagtcacatttcaacataaactctg	1037	
DB	986	CAAGTTTATCAGTCAGCTGGAATGCAACAGTTCA---GTTCTCTTGAACCACCTCTCTT	1042	
QY	1038	tgtataagatccagcgaattctcgaatttttaacaacacttcgcgcctcttcaaattttga	1097	
DB	1043	CAAGTGTTTATGTTGGAAAGCCT---AAAGGAATAATTGTTTGGAGAAACAACGGGATG	1099	
QY	1098	ccacacgcaacatgactcccatctccattcatgtattggcttctgggttggaactcaattatc	1157	
DB	1100	GGACACTTGACATTTCTTGCTCTCTCTGGATGGATTTGTTTTCATGGTGGATTTGCAATTC	1159	
QY	1158	agatcgagcaccacttgttcccaacaatgcccagcttgcaatcgaatcgaatgtcggtgaaat	1217	
DB	1160	AAATTGAGCATCATTTGTTTCCCAGATGCTTAGATGCAACCTTTAGGAAAAATCTCGCCCT	1219	
QY	1218	atgtgaagaatggtgcgaagagaataatctctcttaactcgtcgactactttgacg	1277	

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Db 1220  ACGTGATCGAGTATTGACGAAGAACAATAATTTGCCCTTACAATTATGCATCTTTCTCCAAAGG 1279
Qy 1278  gatatgcaatgaatttgcaacaattgaaataatgctgagcacattccaagctaaagc 1335
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Db 1280  CCAATGAATGACACTCAGAACATTGAGCAACACACAGCATTCGAGGCTAGGATATAAC 1337
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RESULT 6
US-08-366-779-4
; Sequence 4, Application US/08366779
; Patent No. 5614393
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; APPLICANT: Reddy, Avutu S.
; APPLICANT: Nuccio, Michael
; APPLICANT: Freyssinet, Georges L.
; APPLICANT: Nunberg, Andrew N.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; TITLE OF INVENTION: DELTA 6-DESATURASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/366,779

```

```

> FILENAME: 30 DEC 1994
> CLASSIFICATION: 800
> ATTORNEY/AGENT INFORMATION:
> NAME: Presser, Leopold
> REGISTRATION NUMBER: 19,827
> REFERENCE/DOCKET NUMBER: 83832YXW
> TELECOMMUNICATION INFORMATION:
> TELEPHONE: (516) 742-4343
> TELEFAX: (516) 742-4366
> TELEX: 230 901 SANS UR
> INFORMATION FOR SEQ ID NO: 4:
> SEQUENCE CHARACTERISTICS:
> LENGTH: 1685 base pairs
> TYPE: nucleic acid
> STRANDEDNESS: both
> TOPOLOGY: linear
> MOLECULE TYPE: DNA (genomic)
> US-08-366-779-4

Query Match 4.7%; Score 68.4; DB 1; Length 1685;
Best Local Similarity 44.2%; Pred. No. 4.le-09;
Matches 423; Conservative 0; Mismatches 526; Indels 9; Gaps

Qy 381 -cattattcttggttaagcgatttcaacacttccaattatggtcattgcatcttattcttc 440
Db 387 CACTTTTGCTTTATAGCAATGCTGTTTGCATGAGTGTATATGGGGTTTTGTTTGTG 446

Qy 441 agtatcttggtggtatattactcttcgtctgtttattagcacttgcattggcaacaattcg 500
Db 447 AGGCTGTTTTGGTACATTGTTTTCTCGGGTGTTTGTATGGGGTTTCTTTGGATTGAGAGTG 506

Qy 501 gatggttaacacatgatggtctgcatcaacacgcccaacaaagacacagacctttgaatgata 560
Db 507 GTTGAGTTGGACATGATGCTGGGCATTATATGGTAGTGTCTGATTCAGGGCTTAATAAGT 566

Qy 561 ctatttcttctgttgtaattcttacaaggattttcaagagatttggttgaaggaca 620
Db 567 TTATGGGTATTTTTGGTGCAAATGTCCTTTTCAGGAATAAGTATTGCTTTGGTGGAAATGGA 626

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Db 987 CAAAGTTTATCAGTGACTGGAATGCAACAAGTTCA---GTTCTCCTTGAACCACTTCTCTT 1043
Qy 1038 ttgataagtatccagccaattctcgaattttaacaaactccgcgtctctcaaatgtga 1097
Db 1044 CAAAGTGTATGTTGGAAGCCT---AAAGGGAATAAATGGTTTGAGAAACAACCGATG 1100
Qy 1098 ccacagcaaatgactcattccattcattggtggttgggtggaactcaattatc 1157
Db 1101 GGACACTTGACATTTCTTCTCCTCCCTTGGATGGATTGGTTTCATGGTGGATTGCAATTCC 1160
Qy 1158 agatcgagcaccacattgttcccaacaatgccagttgcaatctgaaatctgctggaat 1217
Db 1161 AAATTGAGCATATTGTTTCCACAGATGCCCTAGATGCAACCTTAGGAAAATCTCGCCCT 1220
Qy 1218 atgtgaagaatgggtgcaagagaataatcttccctacactcgcgatgactactttgagc 1277
Db 1221 ACGTGATCGAGTTATGCAAGAACATAAATTTGCCITACAAATATGCATCTTCTCCAAAG 1280
Qy 1278 gatagcaatgaattgcaacaaatgaaataatggtgagcacattcgaagtaaacg 1335
Db 1281 CCAATGAATGACACTCAGAACATTGAGGAACACAGCATTCGAGGCTAGGGATATAAC 1338

RESULT 8

US-08-934-254-4
; Sequence 4, Application US/08934254
; Patent No. 6355861
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; TITLE OF INVENTION: DELTA 6-DESATURASE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,254
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 83832YXWU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1685 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-934-254-4

Query Match 4.7%; Score 68.4; DB 4; Length 1685;
Best Local Similarity 44.2%; Pred. No. 4.1e-09;
Matches 423; Conservative 0; Mismatches 526; Indels 9; Gaps 3;
Qy 381 catatttctgtttaagcagatttcaacactttcaattgaattgagcattgttatcttc 440
Db 387 CAACTTTGTGCTTTATAGCAATGCTGTTTGTCTATGAGTGTATTTATGGGGTTTTGTTGTG 446

Qy 441 agtatcttgatgggtatattacttctgcatgtttattagcacttgcattggtgcaacaattcg 500
Db 447 AGGGTGTGTTGTTGATACATTTGTTCTGGGTGTTTCTGATGGGTTTCTTTGATTCAGAGTG 506
Qy 501 gatggttaacacatgattgcttccatcaacagccaacaagaacagacacctttgaaatgata 560
Db 507 GTTGGATTGGACATGATGCTGGGCATTTATGTTAGTCTGATTCAGGCTTAATAAGT 566
Qy 561 ctatttcttcttcttctgtaatttctcaagagattttcaagagatttctggaagagaca 620
Db 567 TTATGGGTATTTTGTGTCGAAATTTGCTTTCAGGAATAAGTATTTGGTTGGTGAATGGA 626
Qy 621 agcataacactcactcagctgcccacaaatgtaattgatcatgacggtgatactgcacttgg 680
Db 627 ACCATAATGCACATCACATTTGCTGTGAATAGCCTTGAATATGACCTGATTTACAATATA 686
Qy 681 caccactttctgcatttattccaggagattttgcaagataaagccagctttgaaaaag 740
Db 687 TACCATTCTCTGTTGTTGCTCTCCAAAGTTTTTTGGTTTCACTCACTCTCATTTCTATGAGA 746
Qy 741 caattctcaagattgtaccatatacatcaatctctatttaccgcaatgcttc---caatgc 797
Db 747 AAAGGTTGACTTTTGACTCTTTATCAAGATTTCTTTGTAAGTTATCAACATTTGGACATTTT 806
Qy 798 tccgtttctcagactggctcagtcagttcaatgggtatttcaaaagagaatcaaatggagt 857
Db 807 ACCCTATTATGTTGCTGCTAGCTCAATATGATGTATGATACAACTCTCATTAATGTTTGA 866
Qy 858 acaaggtctatcaaaagaaatgattctctgggagcaagcaacaattttgagacattgggctt 917
Db 867 CCAAGAGAAATGTGCTTATCAGCTCAGGAACCTCTTGGGATGCCCTAGTGTCTCTCATTT 926
Qy 918 gggattctcatcaattgttcttattaccacatggccacttcgggttcttatttcatc 977
Db 927 GGTACCCGTTGCTTGTGTTTCTTGTTCCTTAATTTGGGGTGAAGAATATGTTGTTATTG 986
Qy 978 ttccacaaatgggagggccttttgattgctcacgtagtcaactttcaaccataactctg 1037
Db 987 CAAAGTTTATCAGTGACTGGAATGCAACAAGTTCA---GTTCTCTTGAACCACTTCTCTT 1043
Qy 1038 ttgataagtatccagccaattctcgaattttaacaaacttcgcgtctctcaaatgtga 1097
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Qy 1098 ccacagcaaatgactcattccatctcattgattggttgggtggaactcaattatc 1157
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Qy 1218 atgtgaagaatgggtgcaagagaataatcttccctacactcgcgatgactactttgagc 1277
Db 1221 ACGTGATCGATTATGCAAGAACATAAATTTGCTTTACAATATATGATCATCTTTCTCCAAG 1280
Qy 1278 gatagcaatgaattgcaacaaatgaaataatggtgagcacattcgaagtaaacg 1335
Db 1281 CCAATGAATGACACTCAGAACATTGAGGAACACAGCATTCGAGGCTAGGGATATAAC 1338

RESULT 9

US-08-934-254-26
; Sequence 26, Application US/08934254
; Patent No. 6355861
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; TITLE OF INVENTION: DELTA 6-DESATURASE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser

Search completed: August 7, 2002, 02:56:34
Job time: 4820 sec

RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
RA Weitzenecker T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Beineiser S., Hempel S., Feldpausch M., Lamberth S., van den Daele H.,
RA De Keyser A., Buyshaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard-N., McWay K., Mayes R.,
RA Pettitt A., Rajadream M.A., Lyne M., Benes V., Reckmann S.,
RA Borkova D., Bloecker H., Scharf M., Grimm M., Loehner T.-H.,
RA Dose S., de Haan M., Maarse A., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
RA Neumann S., Argirou A., Vitale D., Liguori R., Piravandi E.,
RA Massenot O., Quigley F., Claubold G., Muendlein A., Felber R.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chefford F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Barques M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bieleke C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegler L.,
RA Sehkon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtnay L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Jordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Granat S., Shohdy N., Hasegawa A., Rodriguez M., Hoffman J., Till S.,
RA Chen E., Marra M., Martienssen R., McCombie W.R.,
RA "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RA thaliana";
RT Nature 402:769-777(1999).
RL
CC -1- FUNCTION: CHLOROPLAST OMEGA-6 FATTY ACID DESATURASE INTRODUCES
CC THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC
CC -1- DEVELOPMENTAL STAGE: HIGHEST LEVELS FOUND IN EXPANDING LEAVES.
CC
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U09503; AAA2800.1; -;
CC DR EMBL: AL022198; CAA18198.1; -;
CC DR InterPro: IPR001225; FA_desaturase.
CC DR Pfam: PF00487; FA_desaturase; 1.
CC DR ProDom: PD001081; FA_desaturase; 1.
CC KW Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
CC Transit peptide.
CC TRANSIT 1 69 CHLOROPLAST (BY SIMILARITY).
CC FT CHAIN 70 448 OMEGA-6 FATTY ACID DESATURASE.
CC FT DOMAIN 171 175 HISTIDINE BOX 1.
CC FT DOMAIN 207 211 HISTIDINE BOX 2.
CC FT DOMAIN 367 371 HISTIDINE BOX 3.
CC SQ SEQUENCE 448 AA; 51225 MW; C3AC72FB28BFB287 CRC64;

Query Match

6.9%; Score 165.5; DB 1; Length 448;

Best Local Similarity 23.7%; Pred. No. 1.le-05;
Matches 82; Conservative 60; Mismatches 133; Indels 71; Gaps 19;
QY 88 NVSAVDVSAOEKKWSEFEKLRQKLHDLGMLKMAKETVLEFKALISTLSIMAFAYLQYL 147
Db 104 NVTLDKIDMTLPKEVFEI-----DD--LKALKSVLSVTSYTLGL-----FMAKSP 148
QY 148 WYITSACLLALAWQOFGW-----LTHEFCHQOQTKNRPLNDTI-SLFFGNFLOGFSRD 199
Db 149 WY-----LLPLAWTGTAITGFFVIGHDCAKFSKKNKLVEDIVGTTLAFLPLV--YPVE 201
QY 200 WVKDKNTHHAATNVVIDHGDIDLAPLFAFIPGDLCKYKASEFAKILKIVPQHLYFTAM 259
Db 202 PWREKHDRHRAKTNMLVHD-----TAMQPVPEEFESPMVRKAIL-----FGYGP 248
QY 260 LPMURFS-WTQSGVQWVFKENOMEYKVKYQNR-----AFWEQATIVGHWAWVYQL 308
Db 249 RPWLISIAHW-----VNVHFE--NLKFRASEVNRVKISLACVFAF-----WAVG-WPLIVTKV 297
QY 309 FLPTWPLRVAFYIISQMGGLLIAHVVTFNHNSVDKYPANSRLNFAALQILTRNMT 368
Db 298 GIL-GW---VKFWLMPWLGHYHFWMS-TFTMVHTHTAPHIPKPADEWNAQAQLNGTVHCD 352
QY 369 PSPFIDWMLGGLNVOIEHHLFPTPRCNLNACVKYVKE-WCKENML 413
Db 353 YPSWTEILCHDINVHPIHSPRIPSYNLRAAHESIQENWCKYTNL 398
RESULT 4
FD6C_SP10L STANDARD; PRT; 447 AA.
ID P48629;
AC P48629;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Omega-6 fatty acid desaturase, chloroplast precursor (EC 1.14.99.-).
GN FAD6.
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
[1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 66-78.
RP STRAIN=CV. SUBITO; TISSUE=Leaf;
RX MEDLINE=95036044; PubMed=7948918;
RA Schmidt H., Dresselhaus T., Buck F., Heinz E.;
RT "Purification and PCR-based cDNA cloning of a plastidial n-6
RT desaturase";
RL Plant Mol. Biol. 26:631-642(1994).
CC -1- FUNCTION: CHLOROPLAST OMEGA-6 FATTY ACID DESATURASE INTRODUCES
CC THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X78311; CAA55121.1; -;
CC DR InterPro: IPR001225; FA_desaturase.
CC DR Pfam: PF00487; FA_desaturase; 1.
CC DR ProDom: PD001081; FA_desaturase; 1.

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KW Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
KW Transit peptide.
FT TRANSIT 1 65 CHLOROPLAST.
FT CHAIN 66 447 OMEGA-6 FATTY ACID DESATURASE.
FT DOMAIN 171 175 HISTIDINE BOX 1.
FT DOMAIN 207 211 HISTIDINE BOX 2.
FT DOMAIN 367 371 HISTIDINE BOX 3.
SQ SEQUENCE 447 AA; 51306 MW; 2BA7C87FF95350E CRC64;

Query Match 6.68; Score 158.5; DB 1; Length 447;
Best Local Similarity 20.88; Pred. No. 3.9e-05;
Matches 82; Conservative 60; Mismatches 126; Indels 127; Gaps 18;

Qy 89 VSADVSVAAQE-----KKMVE--SFEKLRKLRKLDHDDGLMK-----AN 122
Db 63 VOAVAVPAQPSAPPDNTTEHLQALAEYGFQIGEPDPDVTMRDIITSLPKQVFEIN 122
Qy 123 EYFELFRAIST--LSIMAF-----FYLOYLGYIITSACLLALAWQOFGW-----LTHEF 170
Db 123 DT----KAWGTVLISVTSYALGIFEMIAKAPWY-----LLPLAWAWTGTAITGFEVIGHDC 173
Qy 171 CHQOPTNRPLNDRI-SLFFGNFLOQFSRDWKKHNTHTHAATNVIDHDGDIDLAPLEAF 229
Db 174 AHKFSKKNKLVEDIVGTALFAPLI--YPYEPWREKHDQHTKTNLRED-----TAW 223
Qy 230 IPGDLCKYKASFKAILEKIVPYQHLFTAMLPMLRFSWTGOSVQWFKENQMEYKVYQRN 289
Db 224 LP--IMKEDISSPLKALIIAY-----GPLRTW-----252
Qy 290 AFWEQATIVGHAWVYQYQ-----FLLPWTPL-----RVAY 320
Db 253 -----SIAHLKVFHFNKDFRQSEVKRATISLAFAFVWIGWPLIIYKTVIGWIKF 305
Qy 321 FIISQMGGLLIAHVFNHNSVDKYPANSRLNFAALQILTRNTMTPSPFIDWLWGLNQTIEHHL 388
Db 306 WLMPLGYHFWMS--TFTIVHHTAPHIPFKSKKEWNAQAQLSGTVHCDYPRWIELCHDI 364
Qy 381 NYQTEHILFTPMPCNLNACVYKKE--WCKENLNP 414
Db 365 SVHPIPHISPIPSYNLRAAQNLSNENWGEVILNKP 399

RESULT 5
FD6C SOYBN STANDARD; PRT; 424 AA.
AC P48628;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
OS Omega-6 fatty acid desaturase, chloroplast precursor (EC 1.14.99.-).
OC Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OC NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seed;
RX MEDLINE=94345008; PubMed=8066133;
RA Hitz W.D., Carlson T.J., Booth J.R., Kinney A.J., Stecca K.L.,
RA Yadav N.S.;
RT "Cloning of a higher-plant plastid omega-6 fatty acid desaturase cDNA
RT and its expression in a cyanobacterium.";
RL Plant Physiol. 105:635-641(1994).
CC -1- FUNCTION: CHLOROPLAST OMEGA-6 FATTY ACID DESATURASE INTRODUCES
CC THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
```


CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC
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CC
CC EMBL; L26296; AAA32782.1; -;
DR EMBL; AP002063; BAB01960.1; -;
DR EMBL; AC069473; AAG51042.1; -;
DR InterPro: IPR001225; FA_desaturase.
DR Pfam: PF00487; FA_desaturase; 2.
DR ProDom: PD001081; FA_desaturase; 1.
KW Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
KW Transmembrane.
FT TRANSMEM 56 76 POTENTIAL.
FT TRANSMEM 117 137 POTENTIAL.
FT TRANSMEM 179 199 POTENTIAL.
FT TRANSMEM 225 243 POTENTIAL.
FT TRANSMEM 252 272 POTENTIAL.
FT DOMAIN 105 109 HISTIDINE BOX 1.
FT DOMAIN 141 145 HISTIDINE BOX 2.
FT DOMAIN 315 319 HISTIDINE BOX 3.
FT SEQUENCE 383 AA; 44047 MW; 8815ADD2D3BBC982 CRC64;

Query Match 5.8%; Score 140; DB 1; Length 383;

Best Local Similarity 21.5%; Pred. No. 0.00091;

Matches 78; Conservative 35; Mismatches 100; Indels 150; Gaps 19;

QY 136 IMAFAFY-----LQYLGW---YITSACLLALAWQFGWLTHFECHQOPTKNR 179
DB 61 IYASCFYVATNTFSLLPQSLYAWPLYWACQGVLTGIWV-----IAHECGHHAFSDYQ 116
QY 180 PLADTISLFFGNFL--QGFSRDWMDKHNTHAATNVIDHDGIDIDLAPLFAFIPGDLCKY 237
DB 117 WLDDTVGLIFHSFLVYPFS---WKYSHRRHSHNTGSLERDE-----VFYP---KQ 161
QY 238 KASFEKAILKIVPYQHLYFTAMLPMLRFSWTGQSVQVFKENOMEXKYVYORNAFWEOATI 297
DB 162 KS-----AIKW-----YCKYLNLP----- 175
QY 298 VGHWAWVYQLFLLPTWPLRVAVFIISQGGGL---LIAHVVTFN-HNSVDKYPANSRI- 352
DB 176 LGRIMMLTVQFVL--GMPLYLAFNVSGRYPDGFACHFPPNAPYNDRERLOIYLSADAGIL 233
QY 353 -----LNNFAALQ-----ILTRNMTSPSFI-----DWLWGG 379
DB 234 AVCFGLYRYAAQGMASMICLYGVPLLIVNAFLVLYLQHTHPSLPHYDSSEMDWLGA 293
QY 380 L-----NQTEHHLFPTMPCNLCNACVYKWKCKENNLVYVDVY - 420
DB 294 LATVDRDYGILNKVFHNITDTHVAHLFSTMPHYNAMEATKAIK-----PILGDYQ 345
QY 421 FDG 423
DB 346 FDG 348

RESULT 8

FD6E_BRAJU

ID FD6E_BRAJU STANDARD; PRT; 384 AA.

AC Q39287;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Omega-6 fatty acid desaturase, endoplasmic reticulum (EC 1.14.99.-)
DE (Delta-12 desaturase).
OS Brassica juncea (leaf mustard) (Indian mustard).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3707;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. 651-2-5-7-4;
RA Singh S.P., van der Heide T., McKinney S., Green A.;
RT "Nucleotide sequence of a cDNA from Brassica juncea encoding a
RT microsomal omega-6 desaturase";
RL (in) Plant Gene Register PGR95-107.
CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-6 FATTY ACID DESATURASE INTRODUCES
CC THE SECOND DOUBLED BOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS (BY SIMILARITY).
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X91139; CAAG2578.1; -;
DR InterPro: IPR001225; FA_desaturase.
DR Pfam: PF00487; FA_desaturase; 2.
DR ProDom: PD001081; FA_desaturase; 1.
KW Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
KW Transmembrane.
FT TRANSMEM 56 76 POTENTIAL.
FT TRANSMEM 84 104 POTENTIAL.
FT TRANSMEM 117 137 POTENTIAL.
FT TRANSMEM 180 200 POTENTIAL.
FT TRANSMEM 226 246 POTENTIAL.
FT TRANSMEM 253 273 POTENTIAL.
FT DOMAIN 105 109 HISTIDINE BOX 1.
FT DOMAIN 141 145 HISTIDINE BOX 2.
FT DOMAIN 316 320 HISTIDINE BOX 3.
FT SEQUENCE 384 AA; 44315 MW; 43AF77CE9861A492 CRC64;

Query Match 5.7%; Score 138.5; DB 1; Length 384;
Best Local Similarity 22.4%; Pred. No. 0.0012;
Matches 78; Conservative 37; Mismatches 114; Indels 119; Gaps 17;

QY 136 IMAFAFY-----LQYLGWYITSAC---LLALAWQFGWLTHFECHQOPTKNR 179
DB 61 IVASCFYVATYTFPLPPLPSYAWPLYWACQGVLTGYVW-----IAHECGHHAFSDYQ 116
QY 180 PLADTISLFFGNFL--QGFSRDWMDKHNTHAATNVIDHDGIDIDLAPLFAFIP---GDL 234
DB 117 WLDDTVGLIFHSFLVYPFS---WKYSHRRHSHNTGSLERDE-----VFYPKKKSDI 165
QY 235 KYKASFEKAILKIVPYQHLYFTAMLPMLRFSWT--GOSVQVFKENOMEXKYVYORNAFW 293
DB 166 KWKYKVLNNPLGRTV-----MLTVQFTLGLWPLWAFNVSGRYPGEGFACHFHP 213
QY 294 QATIVGHWAWVYQLFLLPTWPLRVAV-----FIISQGGGLIAH-----VVT 337
DB 214 NAPIYNDRERL--QIVVSDAGILAVCYGLYRYAAAGVASMVCYGLYVPLLIIVNAFLVLI 271


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CC Bacteria; Cyanobacteria; Oscillatoriales; Spirulina.
OX NCBI_TaxID=1156;
RN [1]
RA Murata N., Deshnlum P., Tasaka Y.;
RP SEQUENCE FROM N.A.
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CAN INTRODUCE A SECOND CIS DOUBLE BOND AT THE DELTA 12
CC POSITION OF FATTY ACID BOUND TO MEMBRANES GLYCEROLIPIDS. THIS
CC ENZYME IS INVOLVED IN CHILLING TOLERANCE BECAUSE THE PHASE
CC TRANSITION TEMPERATURE OF LIPIDS OF CELLULAR MEMBRANES DEPENDS ON
CC THE DEGREE OF UNSATURATION OF FATTY ACIDS OF THE MEMBRANE LIPIDS.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC -----
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CC -----
CC EMBL; X86736; CAA60415.1; -
CC InterPro: IPR001225; FA_desaturase.
CC Pfam: PF00487; FA_desaturase; 1.
CC ProDom: PD001081; FA_desaturase; 1.
CC PROSITE; PS00574; FATTY_ACID_DESATUR_2; FALSE_NEG.
CC OXidoreductase; Fatty acid biosynthesis; Membrane.
CC DOMAIN 89 93 HISTIDINE BOX 1.
CC FT DOMAIN 125 129 HISTIDINE BOX 2.
CC FT DOMAIN 286 290 HISTIDINE BOX 3.
CC FT SEQUENCE 351 AA; 40928 MW; 125A9F1E07E5EE97 CRC64;
CC -----
Query Match 4.6%; Score 110.5; DB 1; Length 351;
Best Local Similarity 21.3%; Pred. No. 0.17;
Matches 64; Conservative 43; Mismatches 121; Indels 73; Gaps 11;

Qy 128 FKATSTLSIMAFYLOVLYWYTSACLLALAW-----QQFGWLTFEFCQQPTKNRP 180
Db 42 YKAMTVTIINVMVGLWGIAIAIPWFLPVVFTGTALTGFVIGHDCGRSFRNVW 101
Qy 181 LNDTIS-LFFGNFLOGFSRDWKKHNTHTAATNVIDHDG-----DIDLAPLFAFIP 231
Db 102 VNDWGHILFLPIIPFHS--WRIGHQHKKYTNRMELDNQWPKRKEEYQNAQFMQVT 159
Qy 232 GDLCYKASFKAALKIVPYQHYLTAMPLMLRFSWTSQSQVW---FKENOMEXKVYQR 288
Db 160 YDLFGR-----WWIGSILHWSIHFDWTKEGKQRQQ 193
Qy 289 NAFWEQATVGHWA-----WVFYQLFLPTWPLRVAYFIISOMGGGLLIAHV 336
Db 194 VKF-SLLVIGAAAFPTMTLTIGVMGFVFWVIP-W-LVFHEWMS-----TF 239
Qy 337 TENHNSVDKYPANSILNFAALQILITRNMTSPFDIWLWGLGNYQIEHLFPTMPCRN 396
Db 240 TLLHHTIADIPFREPEQWHEAESQLSGTVHCNYSRWGEFLCHDINVPHIPHHVTAIPYN 299
Qy 397 L 397
Db 300 L 300

RESULT 13
FD62_SOYBN
ID FD62_SOYBN STANDARD; PRT; 383 AA.
AC P48631.
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Omega-6 fatty acid desaturase, endoplasmic reticulum isozyme 2
DE (EC 1.14.99.-).
DE FAD2-2.
OS Glycine max (Soybean).
```

```
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
CC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RA SEQUENCE FROM N.A.
RP TISSUE=Epicotyl;
RX MEDLINE=96151506; PubMed=8587990;
CC -1- FUNCTION: CAN INTRODUCE A SECOND CIS DOUBLE BOND AT THE DELTA 12
CC POSITION OF FATTY ACID BOUND TO MEMBRANES GLYCEROLIPIDS. THIS
CC ENZYME IS INVOLVED IN CHILLING TOLERANCE BECAUSE THE PHASE
CC TRANSITION TEMPERATURE OF LIPIDS OF CELLULAR MEMBRANES DEPENDS ON
CC THE DEGREE OF UNSATURATION OF FATTY ACIDS OF THE MEMBRANE LIPIDS.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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CC -----
CC EMBL; L43921; AAB00860.1; -
CC InterPro: IPR001225; FA_desaturase.
CC Pfam: PF00487; FA_desaturase; 2.
CC ProDom: PD001081; FA_desaturase; 1.
CC OXidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
CC Transmembrane.
CC FT TRANSMEM 61 81 POTENTIAL.
CC FT TRANSMEM 85 105 POTENTIAL.
CC FT TRANSMEM 117 137 POTENTIAL.
CC FT TRANSMEM 179 199 POTENTIAL.
CC FT TRANSMEM 225 245 POTENTIAL.
CC FT TRANSMEM 249 269 POTENTIAL.
CC FT DOMAIN 105 109 HISTIDINE BOX 1.
CC FT DOMAIN 141 145 HISTIDINE BOX 2.
CC FT DOMAIN 315 319 HISTIDINE BOX 3.
CC FT SEQUENCE 383 AA; 43967 MW; F23EF7159B2F9967 CRC64;
CC -----
Query Match 4.3%; Score 102.5; DB 1; Length 383;
Best Local Similarity 19.7%; Pred. No. 0.8;
Matches 66; Conservative 45; Mismatches 129; Indels 95; Gaps 15;

Qy 124 TYFLFKATSTLSIMAFYLOVLYWYTSACLLALAWQFGWLTFEFCQQPTKNRPLND 183
Db 71 THYFLLPGLPLSFRGMATY-----WAV-QGCILTVWV-----IAHECGHAFESDYQLDD 120
Qy 184 TISLFFGNFL--QGFSDRWKWKDKHNTHTAATNVIDHDGIDLAPLFAFIPGD-----LC 235
Db 121 IVGLILHSALLVPYFS---WKYSHRRHSNTGSLERDE-----VFVKOKSCIKWYS 169
Qy 236 KYKASFEKAILKIVPYQHYLTAML-----PMLRFSWTSQSQVWFKENOMEXKVYQR 288
Db 170 KYLNPPGRLVLTAVTLTGWPLYLALNVSGRPYDFACHYDPYGFYSRE-RLQIYIS 228
Qy 289 NAFWEQATVGHWAIFYOLFLLP-----TWPLRVAYFIISOMGGGLLIAHVVTNNHNS 343
Db 229 DA-----GVLA-VVYGLFLRLAMAKGLAWVVCVGVPLLVVNGFLVLITELQHTHAL 279
Qy 344 DKYPANSRLINNFAALQILITRNMTSPFDIWLWGL-----NYQIE 385
Db 280 PHYTSSE-----WDWLRGALATVDRDYGLLNKVFHNITDTHVA 317
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